


```

Oy      61  ASNLDDDEELCGGLMTLYVLAORMMERLKTIVAGSKMGGLLERVNTLEIHPYTKCAFOPPPSCL 120
Db      61  ASNLDDDEELCGGLMTLYVLAORMMERLKTIVAGSKMGGLLERVNTLEIHPYTKCAFOPPPSCL 120
Oy      121 REVQNTISRLQETSEQLVALKPWITTRONFSRCLTLCQOPDSSLPLPPWSPRPLEATAPT 180
Db      121 REVQNTISRLQETSEQLVALKPWITTRONFSRCLTLCQOPDSSLPLPPWSPRPLEATAPT 180
Oy      181 APQPLLLLLLLLLPVLULLLLAAAMCCHMQTRRTTRRPREQVPVPVSPDQLLVEN 235
Db      181 APQPLLLLLLLLLPVLULLLLAAAMCCHMQTRRTTRRPREQVPVPVSPDQLLVEN 235

RESULT      2
543293
FLTR3/FLK2 ligand (clone S109) - human
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43293
R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Ka-
felt, A.; Muench, M.; Kelnety, G.; Nankakawa, R.; Rennick, D.; Koncarolo, M.G.; Zlotnik, A.
Nature 368, 643-648, 1994
A>Title: Ligand for FLTR3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428
A:Accession: S43293
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-245 <HAN>
A:Note: the authors translated the codon AGT for residue 25 as Met

```

Query Match	69.6%;	Score 864.5;	DB: 2;	Length 245;
Best Local Similarity	73.0%;	Pred. No. 1.1e-66;		
Matches 176;	Conservative	7;	Mismatches 27;	Indels 31;
			Gaps	3;

QY	1	MTVLAPAWSPPTTYLLLLLLLLSSGLSGTODCSFQHSPISSDFAVAKIRELSDYLLQDYPYTV	60
Db	1	MTVLAPAWSPPTTYLLLLLLLLSSGLMGTDQDCSFQHSPISSDFAVAKIRELSDYLLQDYPYTV	60
QY	61	ASNLDDEELCGMLVLAQRMREELKTVASCKKQGLIERNTLHPTKCAPQPPSCL	120
Db	61	ASNLDDEELCGMLVLAQRMREELKTVASCKKQGLIERNTLHPTKCAPQPPSCL	120
QY	121	RFVQNTISRLLQETSEQLVALKPWITRQNFSCLELQCPDSSLPPMSPDELEATAPT	180
Db	121	RFVQNTISRLLQETSEQLVALKPWITRQNFSCLELQCPDSSLPPMSPDELEATAPT	177
QY	181	APQP-----PLLLLLLLPVGLLLLLAAWCMQWQRTRRRTPRCEQYPPVPSR	227
Db	178	WPRPPEGDETAHNGESP-----ARGCIAMTQRLKARGSLPMAPLIPSP	222

QY	228	Q	228
Db	223	E	223

RESULT	3
139076	Flt3 ligand alternatively spliced isoform - human
C:Species:	Homo sapiens (man)
C:Date:	29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession:	139076
A:Flyman, S.D.;	Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S
A:Title:	Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number:	139075; MUID:56032581
A:Accession:	139076
A:Status:	Preliminary; translated from GB/EMBL/DBJ
A:Molecule type:	DNA
A:Residues:	1-178 <RES>
A:Cross-References:	EMBL:U29874; NID:g1072036; PIDN:AAA90950.1; PID:g1072038
A:Introns:	11/3; 48/3; 66/3; 114/3; 161/1
A:Genetics:	

Query Match	67.1%;	Score 834;	DB 2;	Length 178;
Best Local Similarity	100.0%;	Pred. No. 3.3e-64;		
Matches 160;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MTVLPAWSPPTYLLLLLLSSGSGTDCSPQSHSPISDFAVKIRELSDYLLDQYPYTV 60			
Db 1	MTVLPAWSPPTYLLLLLLSSGSGTDCSPQSHSPISDFAVKIRELSDYLLDQYPYTV 60			
QY 61	ASNLDDDELGGIMKLVLAQRMERLKYVAGSKMOGLLERVNTEIHFYTKCAFQPPPSCL 120			
Db 61	ASNLDDDELGGIMKLVLAQRMERLKYVAGSKMOGLLERVNTEIHFYTKCAFQPPPSCL 120			
QY 121	RFVQTNISRLIOETSEOLVALKPWITTRONFSCLCLOCP 160			
Db 121	RFVQTNISRLIOETSEOLVALKPWITTRONFSCLCLOCP 160			

RESULT 4

A49265

flt3/flk-2 ligand precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

A:Accession: A49265; 149347; 149346; S43290

R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl

D.: Williams, D.E.; Beckmann, M.P.

Cell 75, 1157-1167, 1993

A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a

A:Reference number: A49265; MUID:94084791

A:Accession: A49265

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-231 <LV>

A:Cross-references: EMBL:L23636; NID:g439441; PIDN:AAA39436.1; PID:g439442

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581

A:Accession: 149347

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-163, 'G', 165, 'HYAG' <RES>

A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041

A:Accession: 149346

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197, 'L', 198-231 <RE2>

A:Cross-references: EMBL:U29875; NID:g1072039; PIDN:AAA90951.1; PID:g1072040

R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.;

Felt, A.; Muench, J.P.; Kelnier, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik

Nature 368, 643-648, 1994

A:Title: Ligand for flt3/Flk2 receptor tyrosine kinase regulates growth of hematopoiet

A:Reference number: S43230; MUID:94195428

A:Accession: S43230

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197, 'L', 198-231 <HAN>

A:Experimental source: clone T110

A:Note: the sequence from fig. 2c is inconsistent with that from fig. 2a in having 4-

C:Genetics:

A:Introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3

:Keywords: transmembrane protein

	Query Match	61.9%	Score 768.5:	DB 2:	Length 231;
	Best Local Similarity	70.3%:	Pred. No.	1,8e-58:	
	Matches 163; Conservative	17;	Mismatches 43;	Indels 9;	Gaps 4.
QY	1 MTVAPAMPSP--TTTLLILLSSGSLGSFGDCDSFQHPSLSDPAVKYRIRELSDLYLDLPYT	59			
	: : : : :				
bB	1 MTVAPAMPSPNSSLKLLLLLSPLCRGRPDCCYCFHSPPISNNKVRFRETLTHILDKDPVT	60			

```

QY 60 VASNLQDEELCGMLRVLAQRMERLKTAVAGSKMOGLLEEVNTIEHFVTKCAFQPPSPC 119
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 61 VAAVLQDEKRCALMSLFLAQRWIEQLKTAVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
QY 120 LRFVQTNISRLQETSEOLVALKPWITR--QNFSCRLELOCOPDSSSTLPPEMSPPLP 177
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 121 LRFVQTNISRLKDTCTQLALPCIGKACQNFSCRLEVOCCOPDSSSTLPPRSPALFAT 180
QY 178 AAPAPQPP--LILLLLPYGILLAAACLMHQRTRRRTPRPGQVPPVSP 227
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 181 ELPEPRKQILLLLPLTVLAAAGLRMQARRR---GELHPGVPLP 228

```

```

RESULT 5
S43291
PLT3/PLK2 ligand (clone T118) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C/Accession: S43291
R/Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Ka
felt, A.; Muench, M.; Kelnier, G.; Namlkawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A
Nature 368, 643-648, 1994
A/Title: Ligand for FLT3/PLK2 receptor tyrosine kinase regulates growth of haematopoietic
A/Reference number: S43290; MUID:94195428
A/Accession: S43291
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-220 <HAN>

```

```

Query Match 48.8%; Score 606.5; DB 2; Length 220;
Best Local Similarity 61.5%; Pred. No. 1.2e-44;
Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MTVLAPAMSP--TYYLLLLLSGLSGTQDCSFQSHSPISSDPAVKIRLSDVLLQDYVPT 59
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 1 MTVLAPAMSPNSLLLLLLLSPLCLGTPDCYFSHSPISSNKVFRELTHLLKDYPT 60
QY 60 VASNLQDEELCGMLRVLAQRMERLKTAVAGSKMOGLLEEVNTIEHFVTKCAFQPPSPC 119
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 61 VAAVLQDEKRCALMSLFLAQRWIEQLKTAVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
QY 120 LRFVQTNISRLQETSEOLVALKPWITR--QNFSCRLELOCOPDSSSTLPPEMSPPLP 177
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 121 LRFVQTNISRLKDTCTQLALPCIGKACQNFSCRLEVOCCOPDSSSTLPPRSPALFAT 174
QY 174 ---LEATAPAPQPPLL-----LILLPYGILLAA 201
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 175 ATRLTATALLTVCPLPLVGTSHMFLPYFLSPSS 212

```

```

RESULT 6
I58343
fIt3 ligand isoform 5H - mouse
C/Species: Mus sp. (mouse)
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C/Accession: I58343
R/Lyman, S.D.; James, L.; Escobar, S.; Doney, H.; de Vries, P.; Brasel, K.; Stocking, K
Oncogene 10, 149-157, 1995
A/Title: Identification of soluble and membrane-bound isoforms of the murine fIt3 ligand
A/Reference number: I58343; MUID:95124110
A/Accession: I58343
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-220 <RES>
A/Cross-references: GB:S76459; NID:913479; PIDN:AAB33069.1; PID:9913480

```

```

Query Match 48.8%; Score 606.5; DB 2; Length 220;
Best Local Similarity 61.5%; Pred. No. 1.2e-44;
Matches 134; Conservative 18; Mismatches 43; Indels 23; Gaps 5;

QY 1 MTVLAPAMSP--TYYLLLLLSGLSGTQDCSFQSHSPISSDPAVKIRLSDVLLQDYVPT 59

```

```

Db 1 MTVLAPAMSPNSLLLLLLLSPLCLGTPDCYFSHSPISSNKVFRELTHLLKDYPT 60
QY 60 VASNLQDEELCGMLRVLAQRMERLKTAVAGSKMOGLLEEVNTIEHFVTKCAFQPPSPC 119
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 61 VAAVLQDEKRCALMSLFLAQRWIEQLKTAVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
QY 120 LRFVQTNISRLQETSEOLVALKPWITR--QNFSCRLELOCOPDSSSTLPPEMSPPLP 177
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 121 LRFVQTNISRLKDTCTQLALPCIGKACQNFSCRLEVOCCOPDSSSTLPPRSPALFAT 174
QY 174 ---LEATAPAPQPPLL-----LILLPYGILLAA 201
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 175 ATRLTATALLTVCPLPLVGTSHMFLPYFLSPSS 212

```

```

RESULT 7
T22672
hypothetical protein F54F12.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T22672
R/Barlow, K.
Submitted to the EMBL Data Library, November 1996
A/Reference number: Z19597
A/Accession: T22672
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1217 <ML>
A/Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CA804464.1; GSPDB:GN00021; CESP:F
A/Experimental source: clone F54F12
A/Map position: 3
A/Genes: CESP:F54F12.1
A/Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

```

```

Query Match 7.5%; Score 93; DB 2; Length 1217;
Best Local Similarity 23.6%; Pred. No. 8;
Matches 38; Conservative 33; Mismatches 68; Indels 22; Gaps 6;

QY 83 MERLKTAVAGSKMOGL---LERYNTEIHFVTKCAFQPPSPCLRFVQTNISRLQETSDQV 139
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 627 MDKAVKAVDGTKSSVIDALEKSLMDLDFQKKYKFEADATLKAMDL---FFASVSNLA 682
QY 140 ALKPMWTRONFSRCLELOCOPDSSSTL---PPPMSPRLPENTAPAP---QPLLLLL 191
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 683 ALRPPQPTSDPTAABVPPIPNKKSILNGNPSPPSPLLPVVAASSTPAATPESSNMLYTI 742
QY 192 LPVGLLLAA-----AWCLHMQRTRRRTPRPGQVPPVSP 227
  ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| ||| : ||| |||
Db 743 GAVGGLLVAAIGVILFEVFQKKKKKKEDKPD--PPAPLP 781

```

```

RESULT 8
TINB12
74K alpha trans-inducing protein - human herpesvirus 3
C/Species: human herpesvirus 3, varicella-zoster virus
C/Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C/Accession: C27342
R/Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A/Title: The complete DNA sequence of varicella-zoster virus.
A/Reference number: A27345; MUID:8630657
A/Accession: C27342
A/Molecule type: DNA
A/Residues: 1-661 <DAV>
A/Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27895.1; PID:g60001
C/Genetics:
A/Genes: 12
C/Superfamily: herpesvirus 77K alpha trans-inducing protein
C/Keywords: trans-inducing protein; transcription regulation

```


C:Species: Drosophila melanogaster
C>Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
C:Accession: A32290; S12008
R:Edgar, B.A.; O'Farrell, P.H.
Cell 57, 177-187, 1989
A:Title: Genetic control of cell division patterns in the Drosophila embryo.
A:Reference number: A32290; MUID:89195217
A:Accession: A32290
A:Molecule type: mRNA
A:Residues: 1-479 <EDC>
A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508
R:Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
EMBO J. 9, 3565-3571, 1990
A:Title: Complementation of fission yeast cdc2(ts) and cdc25(ts) mutants identifies two
A:Reference number: S12008; MUID:91006056
A:Accession: S12008
A:Molecule type: mRNA
A:Residues: 1-227, 'A', 229-479 <JIM>
A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707
C:Genetics:
A:Gene: FlyBase:sg
A:Cross-references: FlyBase:FBgn0003525
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and
A:Pathway: Initiation of mitosis
A>Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it
C:Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphat
C:Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase;
F:25-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <PPP>
F:379/Active site: Cys (phosphocysteine intermediate) #status predicted
F:385/Binding site: substrate phosphate (Arg) #status predicted

Query Match 7.0%; Score 87.5; DB 1; Length 479;
Best Local Similarity 22.9%; Pred. No. 8.2;
Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;
OY 1 MTVALPAMSPPTLYLL---LLLSGSLGTQDCSFQHSPISSDPAVAVIRELSVLLQDYP 57
Db 72 MGLSPBSSPQRFQIVROPKLTPMAGVSS-----DHTPARS-FRI-FNSLSS-----T 117
OY 58 VTVASNLQDEELCGMLWVLAQRMERLKTAVAGSKMGLLEVRNTEIHFTKCAFGQPP 117
Db 118 CSMSSMODE-----YMELFEMESQ-----QTALGF-----P 146
OY 118 SCLRPVQTNISRLIQETSEQLVAKP---WTRQNFSCRLEL-QCQPDSSTLPPWSPRP 173
Db 147 SGLN-----SLISGOIKQEPAPAKSPAGLSMRPSVRCLSMTEBSNTSTTPPKTPE- 199
OY 174 LEATAPTA---POPLRLLLLLLPVGLLLAAMCLHMQRRTRRPRRGEQVPPVPSQDL 230
Db 200 ---TARDCEKRPPE-----ASANCSPIOSKRHRCAVKEKENCAPSPLSQ 242
OY 231 LLVER 235
Db 243 VTISH 247
RESULT 16
A53137
tyrosine kinase receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A53137
R:Sanchez, M.P.; Tapley, P.; Saini, S.S.; He, B.; Pulido, D.; Barbacid, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 1819-1823, 1994
A:Title: Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Pk-
A:Reference number: A53137; MUID:94173920
A:Accession: A53137
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-910 <RES>
A:Cross-references: GB:L26525; NID:g432480; PIDN:AAA1089.1; PID:g432481

C:Genetics:
A:Gene: Pk-3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-
C:Keywords: ATP
F:31-186/Domain: discoidin I amino-terminal homology <DN1>
F:605-909/Domain: protein kinase homology <KIN>
F:613-621/Region: protein kinase ATP-binding motif

Query Match 7.0%; Score 87; DB 2; Length 910;
Best Local Similarity 24.5%; Pred. No. 19;
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;
OY 143 PWTRQNFRCLELQCPDSTLP-PW---SPRPLEATA---PTADP----- 184
Db 356 PWLFEISFISDV-VNDSDFPPAPMWPQGPPTNFSLLEPRGQPPVAKAGSPTA 414
OY 185 -----PLLILLPLPVGLLLAAMCLMQR-----TRRR-----T 214
Db 415 ILIGLVAITILLITLITLML---WRLHWRRLSKAERRVLEELTVHLSVPGDTILIN 470
OY 215 PRPEQVPP-----VPSPODLL 232
Db 471 NRPGRPEPPYQRPGRGTHSAPCVPGSALL 505

RESULT 17
A40437
glutamic acid-rich protein, retinal - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
C:Accession: A40437
R:Sugimoto, Y.; Yatsunami, K.; Tsujimoto, M.; Khorana, H.G.; Ichikawa, A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3116-3119, 1991
A:Title: The amino acid sequence of a glutamic acid-rich protein from bovine retina
A:Reference number: A40437; MUID:91195303
A:Accession: A40437
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-590 <SDG>
A:Cross-references: GB:M61185; NID:g163077; PIDN:AAA30536.1; PID:g163078

Query Match 7.0%; Score 86.5; DB 2; Length 590;
Best Local Similarity 24.6%; Pred. No. 13;
Matches 35; Conservative 13; Mismatches 53; Indels 41; Gaps 5;
OY 115 PPSCLRFQVQTNISRL-----QETSQVATKPWITRQNFRCLE 154
Db 163 PGFWLRFMEQNLKMLPQPKRISGWRDEPTDALGPPPEPALEIKPMLOAO----- 216
OY 155 ELQCPDSSSTLPWSPRPLENTAFAPQPLLLLLLPVGLLLAAMCLHMQRTRRT 214
Db 217 -----ESPSLPAPGPPEEERIP-EPQPTIQASSLPPQDSARLMMIILH-RLEMAL 267
OY 215 PRP-----GEQVPPVPSQDL 230
Db 268 PQPVIRKKGEOESDAPVTCOV 289

RESULT 18
T17832
hypothetical protein A333L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17832
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: T17832
A:Accession: T17832
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-299 <GRA>

R:Simister, N.E.; Mostov, K.E.

Nature 337, 184-187, 1989

A:Title: An Fc receptor structurally related to MHC class I antigens.

A:Reference number: S02117; MUID:89097257

A:Accession: S02117

A:Molecule type: mRNA

A:Residues: 1-366 <S12>

A:Cross-references: EMBL:X14323; NID:956436; PIDN:CAA32503.1; PID:956437

A:Note: part of this sequence, including the amino end of the mature protein, was confli

C:Superfamily: class I histocompatibility antigen: immunoglobulin homology

C:Keywords: immunoglobulin receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-366/Product: IgG Fc receptor 51k chain #status predicted <MAT>

Query Match 6.8%; Score 85; DB 2; Length 366;

Best Local Similarity 22.2%; Pred. No. 9.9;

Matches 51; Conservative 21; Mismatches 66; Indels 92; Gaps 11;

QY 46 RELSDYLQDPYTVASNLQDELICGGLMRLVLAQRWME---RLKTVAGSKMGGLEERV 101

Db 173 RKESEFLLTSCP-----ERLLGHLERGRQMLEWKEPPSMRLKARPGNSGSSVL--- 220

QY 102 NTEIHFTYKCA--FQPPSCIRFVQTNISRLQETSEQLVALKPWITRQNFSC----- 153

Db 221 -----TCAAFSFTPELKFRLKNGLA-----SGSGMCSGEPN 253

QY 154 -----LEL-----QCQPDSSSTLPWPSPRPLEATAPARQPLLLLPVG 195

Db 254 GDGSFHAMSLLEVKRGDEHHQCQVEHGLAQPLT---VDDLSPARSSVPPVGIIL---G 307

QY 196 LLILIA---AAMCLHWQTRRRTPR-----PGQVPPVPVSPQ 228

Db 308 LLILVVAIAGGVLLMNRMRGSLPAPWLSLSCGDSGDLPGGNLPPEAEAPQ 357

RESULT 23

tegument protein 67 - alcelaphine herpesvirus 1

C:Species: alcelaphine herpesvirus 1

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999

C:Accession: T03162

R:Esser, A.; Pfanz, R.; Fleckenstein, B.

J. Virol. 71, 6517-6525, 1997

A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.

A:Reference number: 214840; MUID:97404659

A:Accession: T03162

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-263 <ENS>

A:Cross-references: EMBL:AF005370; NID:92337967; PIDN:AAC58114.1; PID:92338030

C:Superfamily: human herpesvirus 4 BRF1 protein

Query Match 6.8%; Score 84; DB 2; Length 263;

Best Local Similarity 25.3%; Pred. No. 8.3;

Matches 55; Conservative 30; Mismatches 84; Indels 48; Gaps 10;

QY 8 WSPPTVLLILLSSGSGTQDCSFQHSPISSDAVAKIRELSDVILQDPYTVASNLQDE 67

Db 77 FSPF-----FTCNNGLAIVLK-----YSEPRDLSRYGQATSNALVYNLQRN 121

QY 68 ELGGLMRLVLAQRWME---VAGSKM--OGLLERVNTIEHFVTCARQPP 116

Db 122 SF-----VVLSDQDFIKFTPLVFAKDDITNSMVVCRTVLTSSRNSLQFLV--VSKN 173

QY 117 PSCLRFVQTNISRLQETSEQLVALKPWITRQNFSCLEL--QCQPDSSSTLPWPSPRPLE 175

Db 174 PRRLENIWDMIKRAVEATGSLPA-----TPE---KPLPLEQTEQLSTLPSGHLRLVQ 225

QY 176 ATAPTAQPP-----LLILLPLVGLLLIAAACLHW 207

Db 226 STSLTGRCPSMGACALLLLSLAVGMAIILAKIMQW 262

RESULT 24

gamma-glutamyl carboxylase (EC 4.1.1.-) - human

A39283

C:Species: Homo sapiens (man)

C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 06-Dec-1996

C:Accession: A39283

R:Wu, S.M.; Cheung, W.F.; Frazier, D.; Stafford, D.W.

Science 254, 1634-1636, 1991

A:Title: Cloning and expression of the cDNA for human gamma-glutamyl carboxylase.

A:Reference number: A39283; MUID:92086858

A:Accession: A39283

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: mRNA

A:Residues: 1-757 <WTA>

A:Cross-references: GB:M81592

C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 6.8%; Score 84; DB 2; Length 757;

Best Local Similarity 22.3%; Pred. No. 28;

Matches 50; Conservative 29; Mismatches 59; Indels 86; Gaps 13;

QY 3 VLAAMSPTTLLLLSSGSGTQDCSFQHS---PISDFA---VKIRELSDYL--- 52

Db 488 IVQAAWSP-----FQRTSWQVPLNDLSPPWRAKLOEIKSSLDNN 526

QY 53 -----LQDPYTVASNLQDELICGGLMRL-----VLAQRWMERLKTVAGSKMQ--G 96

Db 527 TEVVFADFPGLNLENVSEDLGNTSTQLQGEVTVELVAQKQKQTL--BGEKMQLPAG 584

QY 97 LLERVNTEHFVTCARQPPSCIRFVQTNISRL-----LQETSEQLVALKPWITRQ 148

Db 585 EYKNVYTT-----SPSPCYMYVYVNTTELAEQDLAYLOELKEKY-----E 626

RESULT 25

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: E75630

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

M.; Shen, M.; Yamanehan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: E75630

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-199 <MID>

A:Cross-references: GB:AE001826; NID:96460827; PIDN:AAF12655.1; PID:96460951; TIGR:DR

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRB0112

A:Map position: megaplasmid

A:Genome: plasmid

A:Note: plasmid MP1

Query Match 6.7%; Score 83.5; DB 2; Length 199;

Best Local Similarity 27.3%; Pred. No. 6.6;

Matches 47; Conservative 29; Mismatches 57; Indels 39; Gaps 13;

QY 75 RLTVLAQR--WMERLKTVAGSKMGGLEERVNTEHFVTCARQPPSCIRFVQTNISRLQ 133

Db 50 RLSTQRTWQQTALITRSQVRSYSDR-----HGV--MTQPD--VTYVYQSGR----- 94

```

QY 134 TSEQLVAKPWITRONFS---RCLELOCQP--DSTLPPPMSPR--ELEATAPTAQPP 185
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 95 -NYGIALDP-LSDNNYRFSFNAYQRSIQPYQESTVPLFYEDPONPGQSALSILTRSTPP 152
QY 186 LLLLL-----LLPYGILLAAACLIHQTRRR--TPRGEQ-VPVPSPQD 229
   | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 153 LSLMLGVTFELGLGSLIGARM---RTKRROIYTKPGHODAKGSPGPRD 199

```

Search completed: August 6, 2002, 09:40:23
 Job time: 214 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:39:39 ; Search time 16.81 Seconds
(without alignments)
541.291 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MRYLAPMSPTTYLLLLLL.....RPGQVPPVSPQDLLVEH 235

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1242	100.0	235 1 FL3L_HUMAN	P49771 homo sapien
2	768	61.8	232 1 FL3L_MOUSE	P49772 mus musculu
3	92	7.4	661 1 AT12_VYVD	P09264 varicella-z
4	89.5	7.2	941 1 GBR2_HUMAN	O75899 homo sapien
5	89	7.2	387 1 SGCA_MESAU	O64255 mesocricetu
6	89	7.2	793 1 S3A1_HUMAN	O15459 homo sapien
7	87.5	7.0	415 1 TNF3_MOUSE	P50284 mus musculu
8	87.5	7.0	479 1 MPTP_DROME	P20483 drosophila
9	87	7.0	910 1 DDRI_RAT	O63474 rattus norv
10	87	7.0	911 1 DDRI_MOUSE	O03146 mus musculu
11	86.5	7.0	1394 1 CNG4_BOVIN	O28181 bos taurus
12	86	6.9	485 1 SSGP_VOLCA	P21997 volvox cart
13	85	6.8	282 1 ATFS_HUMAN	O949d1 homo sapien
14	85	6.8	366 1 FCCN_RAT	P13599 rattus norv
15	84.5	6.8	3726 1 ABR1_MOUSE	O61329 mus musculu
16	84	6.8	582 1 MNT_MOUSE	O99583 homo sapien
17	84	6.8	732 1 YF48_HUMAN	O99m4 homo sapien
18	83.5	6.7	671 1 Z282_HUMAN	O9uav7 homo sapien
19	83	6.7	758 1 VKGC_HUMAN	P38435 homo sapien
20	81.5	6.6	488 1 MMT1_MOUSE	P24347 homo sapien
21	81.5	6.6	591 1 MNT_MOUSE	O08789 mus musculu
22	81.5	6.6	2124 1 IY97_HUMAN	O93074 homo sapien
23	81	6.5	283 1 ATFS_MOUSE	O70191 mus musculu
24	81	6.5	387 1 SGCA_MOUSE	P82350 mus musculu
25	81	6.5	428 1 EPC_HUMAN	P01854 homo sapien
26	81	6.5	1248 1 DIAL_HUMAN	O06010 homo sapien
27	80.5	6.5	1402 1 IF4G_RABIT	P41110 cyrtolaqus
28	80	6.4	397 1 CEFD_STRCL	P18549 strepomyces
29	80	6.4	940 1 GBR2_RAT	O88871 rattus norv
30	80	6.4	1174 1 KPCI_COCHF	O42632 cochliobolu
31	80	6.4	1794 1 YAVI_SCHPO	O10172 schizosach
32	79	6.4	805 1 YGW6_YEAST	P53086 saccharomyc
33	78.5	6.3	251 1 HXB4_HUMAN	P17483 homo sapien

34	78.5	6.3	382 1 AVR8_RAT	P38445 rattus norv
35	78.5	6.3	387 1 SGCA_RABIT	O28686 oycyclolagus
36	78.5	6.3	913 1 DDRI_HUMAN	O08345 h epithelia
37	78.5	6.3	1180 1 ATY1_HUMAN	O9ng1 homo sapien
38	78	6.3	205 1 CYSR_SYNY3	O55854 synechocyst
39	78	6.3	566 1 TS13_MOUSE	O01755 mus musculu
40	77.5	6.2	1885 1 FAS2_CANAL	P43098 c fatty aci
41	77.5	6.2	2004 1 MO2_HUMAN	O27794 homo sapien
42	77	6.2	195 1 CORA_HPBVF	P29178 hepatitis b
43	77	6.2	316 1 CDNC_HUMAN	P49318 homo sapien
44	77	6.2	367 1 MREC_ECOLI	P16926 escherichia
45	77	6.2	478 1 BM3B_HUMAN	P55107 homo sapien
46	77	6.2	742 1 PKWA_THECU	P49695 thermomnos
47	77	6.2	872 1 SYV_HELPY	O92k61 helicobacte
48	76.5	6.2	362 1 OPRR_CHICK	P22329 gallus gall
49	76.5	6.2	498 1 MEFA_MOUSE	O60923 mus musculu
50	76	6.1	190 1 BCT7_SHEEP	P50415 ovis aries

ALIGNMENTS

RESULT 1	FL3L_HUMAN	STANDARD:	PRT: 235 AA.
ID	FL3L_HUMAN		
AC	P49771;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLT3 ligand).		
CN	FL3LUC.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94195428; PubMed=8145851;		
RA	Hannun C., Culppeper J., Campbell D., McClanahan T., Zurawski S.,		
RA	Bazan J.F., Kastelein R., Hudak S., Wagner J., Matson J., Luh J.,		
RA	Duda G., Matlika N., Peterson D., Menon S., Shanalelt A.,		
RA	Mench M., Relner G., Namiikawa R., Rennick D., Roncarolo M.G.,		
RA	Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;		
RT	"Ligand for FLT3/PLK2 receptor tyrosine kinase regulates growth of		
RT	hematopoietic stem cells and is encoded by variant RNAs.";		
RL	Nature 368:643-646(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94235842; PubMed=8180375;		
RA	Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,		
RA	Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.;		
RT	"Cloning of the human homologue of the murine flt3 ligand: a growth		
RT	factor for early hematopoietic progenitor cells.";		
RL	Blood 83:2795-2801(1994).		
RN	[3]		
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.		
RX	MEDLINE=96032581; PubMed=7566977;		
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,		
RA	Escobar S.;		
RT	"Structural analysis of human and murine flt3 ligand genomic loci.";		
RL	Oncogene 11:1165-1172(1995).		
CC	-1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC		
CC	CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING		
CC	FACTORS AND INTERLEUKINS.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM		
CC	IS ALSO PRODUCED BY ALTERNATIVE SPLICING.		
CC	-1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE		
CC	SPLICING.		
CC	-----		
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DR EMBL; U03806; AAA1799.1; -
DR EMBL; U03858; AAA19825.1; -
DR EMBL; U29874; AAA90949.1; -
DR EMBL; U29874; AAA90950.1; -
DR MIM; 600007; -
DR InterPro: IPR004213; flt3_1lg.

DR Pfam; PF02947; flt3_1lg, 1.
KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
FT SIGNAL 1 26
FT CHAIN 27 235
FT DOMAIN 27 184
FT TRANSMEM 185 205
FT DOMAIN 206 235
FT CARBOHYD 126 126
FT CARBOHYD 149 149
FT VARSPIC 161 178
FT VARSPIC 179 235
FT CONFLICT 72 72
FT SEQUENCE 235 AA; 26416 MW; 73B95BF693B4CCEFCRC64;
Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAPMSPTTYLLDLLLSGSGISGQDSFQHSPISSDPFAKIRELSIDYLLQDYPVY 60
DB 1 MTVALPAPMSPTTYLLDLLLSGSGISGQDSFQHSPISSDPFAKIRELSIDYLLQDYPVY 60
QY 61 ASNQDEPLCGIMRLVLAQRMRERLKTAVGSKMGGILEVNEIHFVTKCAQPPPSCL 120
DB 61 ASNQDEPLCGIMRLVLAQRMRERLKTAVGSKMGGILEVNEIHFVTKCAQPPPSCL 120
QY 121 RFVQTNISRLQETSEDLVALKPIWTRQNFSCLELOCOPDSTLPPSPRPLEATAPY 180
DB 121 RFVQTNISRLQETSEDLVALKPIWTRQNFSCLELOCOPDSTLPPSPRPLEATAPY 180
QY 181 APOPPILLLLPYGILLIAAMCLHMQRRTPRGEGVPPVPSPOLLYVEH 235
DB 181 APOPPILLLLPYGILLIAAMCLHMQRRTPRGEGVPPVPSPOLLYVEH 235

RESULT 2
FL3L_MOUSE STANDARD; PRT; 232 AA.
ID FL3L_MOUSE
AC P49772;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLT3 DE ligand).
GN FLT3LG OR FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; Pubmed=8145851;
RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Buzan J.F., Kastelein R., Hudak S., Wagner S., Matsson J., Luh J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kellner G., Nankawa K., Kennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubrenil P., Birnbaum D., Lee F.;
RT "Ligand for FLT3/FLT3 receptor tyrosine kinase regulates growth of hematopoietic stem cells and is encoded by variant RNAs.";
RL Nature 368:643-648(1994).

RN [2]
RP SEQUENCE FROM N.A.
RC SRRAIN-SL/7;
RX MEDLINE=94084791; Pubmed=7505204;
RA Lyman S.D., James L., Vandenbos T., Devries P., Brasel K., Gliniak B., Hollingsworth L.T., Picha K.S., McKeena H.J., Splet R.R., Fletcher F.A., Maraskovsky E., Farrah T., Foxworth D., Williams D.E., Beckmann M.P.;
RT "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a proliferative factor for primitive hematopoietic cells.";
RL Cell 75:1157-1167(1993).

RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96032581; Pubmed=7566977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L., Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).

RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95124710; Pubmed=7824267;
RA Lyman S.D., James L., Escobar S., Downey H., de Vries P., Brasel K., Stocking K., Beckmann M.P., Copeland N.G., Cleveland L.S.;
RT "Identification of soluble and membrane-bound isoforms of the murine flt3 ligand generated by alternative splicing of mRNAs.";
RL Oncogene 10:149-157(1995).

RN [5]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K., Matsson J., Tsai S., Luh J., Guimares M.J., Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.;
RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.

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CC EMBL; U04807; AAA18000.1; -
DR EMBL; U23636; AAA39436.1; -
DR EMBL; U29875; AAA90951.1; -
DR EMBL; U29875; AAA90952.1; -
DR EMBL; U29875; AAB33069.1; -
DR EMBL; S76459; AAB33069.1; -
DR EMBL; S76461; AAB33070.1; -
DR EMBL; U44024; AAA93307.1; -
DR EMBL; U44024; AAA93306.1; -
DR MGD; MGI:95560; Flt3l.
DR InterPro: IPR004213; flt3_1lg, 1.
DR Pfam; PF02947; flt3_1lg, 1.
KW Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
FT SIGNAL 1 26
FT CHAIN 27 232
FT DOMAIN 27 189
FT TRANSMEM 190 210
FT DOMAIN 211 232
FT CARBOHYD 127 127
FT CARBOHYD 152 152
FT VARSPIC 164 232
FT VARSPIC 164 169
FT CONFLICT 164 169
FT SEQUENCE 164 169
Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 3e-97;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Mesocricetus.
 OX NCBI_Taxid=10036;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=STRIAN; TISSUE=Heart muscle;
 RA MEDLINE=98054328; PubMed=9391120;
 RA Sakamoto A., Ono K., Abe M., Jamin G., Eki T., Murkami Y.,
 RA Masaki T., Toyooka T., Hanaoka F.;
 RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation
 RT of the same gene, delta-sarcoglycan, in hamster: an animal model of
 RT disrupted dystrophin-associated glycoprotein complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FLB; TISSUE=Skeletal muscle;
 RA MEDLINE=95278335; PubMed=7758576;
 RA Roberts S.L., Campbell K.P.;
 RT "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic
 RT hamster.";
 RL FEBS Lett. 364:245-249(1995).
 CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF
 CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE
 CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SARCOLEMMA
 CC (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND
 CC HEART MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
 CC
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 CC
 DR EMBL; D83651; BAAL2025.1; -
 DR EMBL; U21677; AAA81645.1; -
 KW Cytoskeleton; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 387
 FT DOMAIN 24 290 ALPHA-SARCOGLYCAN.
 FT TRANSSEM 291 311 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 312 387 POTENTIAL.
 FT DOMAIN 209 335 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 174 174 CYS-RICH.
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;

Query Match 7.28; Score 89; DB 1; Length 387;
 Best Local Similarity 23.48; Pred. No. 2.3;
 Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYLLLLSSGLSTGDSFQHSPISSDFAVKIRELSIDYLLQDVPYVASMLODEELC 70
 DB 115 TTRGRLLLLT-----EDDEGPRILPYQAEFLVRSNDVEVL-----PSTPANRFL--TAL 161
 QY 71 GGIWRL-----VLAQRMERLKTVAAGSKMGLLEERVTETHEFT-----K 110
 DB 162 GGIMELGELOLLNITSALDRGGRVPLPIEGRKEGYIKVGSAPPFSTCLKMAVSPDSYAR 221
 QY 111 CARQPP--SC-----LRFVGTNISRLQLQHSSEDLVALKPMITQNSRCELOCQPD 161
 DB 222 CAAGQPPILSCYSLAPHFVDMCNVSLVDKSVPEPID-----EVPDPD 266
 QY 162 SSTLPWPWSRPLEAT-----APTAPQPPILLLLLPVGLLLAAMC----- 204
 DB 267 GILEHDPFCPPPEATGRDPLADALVTLVPLLVALL--TLLAVYIMCRRREGOLKRD 323
 QY 205 -----LHMQRTRRRTPR-----GQVPP-VSPQ-DLL 231

DB 324 MATSDIQMVHCHTIGHNTEBLROMAARREVPRLSTLPWFNVRTGERLPDPRVDSAQVPLI 383
 QY 232 LVEN 235
 DB 384 LDQH 387
 RESULT 6
 S3AL_HUMAN
 ID S3AL_HUMAN STANDARD; PRT; 793 AA.
 AC O15459;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 01-MAR-2002 (rel. 41, Last annotation update)
 DE Splicing factor 3 subunit 1 (spliceosome associated protein 114) (SAP
 DE 114) (SF3A120).
 GN SF3A1 OR SAP114.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079958; PubMed=7489498;
 RX Kraemer A., Kulhauser F., Weisig C., Groning K., Bilbe G.;
 RT "Mammalian splicing factor SF3A120 represents a new member of the
 RT SURP family of proteins and is homologous to the essential splicing
 RT factor PRP21p of Saccharomyces cerevisiae.";
 RL RNA 1:260-272(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RX Dunham I., Hunt A.R., Collins J.E., Bruskielich R., Beare D.M.,
 RA Clamp M., Smink L.J., Alnscoough R., Almeida J.P., Babbage A.,
 RA Baguley S., Bailey J., Barlow K., Bates K.N., Beasley O., Bird C.P.,
 RA Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M.,
 RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., Corby N.,
 RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
 RA Dowdworth S.J., Durbin R.M., Ellington A., Evans K.L., Fey J.M.,
 RA Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E.,
 RA Grahnam D., Griffiths M.N., Hall C., Hall R., Hall-Remyn G.,
 RA Heathcott R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Keshaw J.,
 RA Kimberley A., King A., Laird G.K., Langford C.F., Leverha M.A.,
 RA Lloyd C., Lloyd D.M., Marlyn I.D., Mashneghi-Mohammadi M.,
 RA Matthews L., Mccann O.T., Mccloy J., Mclaren S., Mcmurray A.A.,
 RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
 RA Pearson D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsay H.,
 RA Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Skuce C.D.,
 RA Smalley S., Smith M.L., Soderlund C., Spragon L., Stewart C.A.,
 RA Sulton J.E., Swann R.M., Vaudin M., Walli M., Wallis J.M.,
 RA Whiteley M.N., Willey D., Williams L., Williams S., Williamson H.,
 RA Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R.,
 RA Beck S., Rogers J., Shimizu N., Minooshima S., Kawasaki K., Saeki T.,
 RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshitaki Y., Aoki N.,
 RA Mitsuyma S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S.,
 RA Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S.,
 RA Lai H., Lao H.I., Lewis J., Lewis S., Jin S.-P., Loh P., Malaj E.,
 RA Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
 RA Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D.,
 RA Wu H., Yao Z., Zhan M., Zhang G., Chisose S., Murray J., Miller N.,
 RA Mix P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H.,
 RA Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T.,
 RA Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozerisky P.,
 RA Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K.,
 RA Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurehashi H., Salita S.,
 RA Budarf M.L., Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
 RA Peyrard M., Kedia D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tilihan Y., Wright H.;
 RT "The DNA sequence of human chromosome 22.";

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RL Nature 402:489-495(1999).
RN [3]
RP CHARACTERIZATION OF THE SPLICEOSOME.
RX MEDLINE=20337962; PubMed=10882114;
RA Das R., Zhou Z., Reed R.;
RT "Functional association of U2 snRNP with the ATP-independent
RT spliceosomal complex E.";
RT Mol. Cell 5:779-787(2000).
CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
CC ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP114. SF3A
CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
CC INTERACTS WITH SF3A3.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.
CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
CC -----
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CC -----
DR EMBL; X85237; CAA59494.1; -
DR EMBL; AC004997; AAC23435.1; -
DR MIM: 605595; -
DR InterPro: IPR000061; Surp.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF01805; Surp; 2.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART; SM00213; UBO; 1.
DR PROSITE; PS50053; UBQUITIN_2; 1.
DR Spliceosome; mRNA processing; Nuclear protein; Repeat.
KW REPEAT
FT REPEAT 52 94
FT REPEAT 166 208 SURP MOTIF 2.
FT DOMAIN 707 793 UBQUITIN-LIKE.
FT DOMAIN 10 16 POLY-PRO.
FT DOMAIN 118 122 POLY-GLN.
FT DOMAIN 260 267 POLY-GLU.
FT DOMAIN 369 372 POLY-PRO.
FT DOMAIN 557 560 POLY-PRO.
FT DOMAIN 672 675 POLY-PRO.
SQ SEQUENCE 793 AA; 88886 MW; 725991EC4577305C CRC64;

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OY 146 -----SRCTLEOCOP-----DSSTLP-----PPWSRPLEAT-----APT 180
OY 146 -----SRCTLEOCOP-----DSSTLP-----PPWSRPLEAT-----APT 180
DB 537 PEDTKEKIGSKPNEIPQDPPPPSSATNIPSSAPITTSVPRPTMPPTVIVSAVPV 536
DB 537 PEDTKEKIGSKPNEIPQDPPPPSSATNIPSSAPITTSVPRPTMPPTVIVSAVPV 536

Query Match 7.28; Score 89; DB 1; Length 793;
Best Local Similarity 22.38; Pred. No. 5.1;
Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

OY 4 LAPAMSPYTLILLILLSSGLSTQDSFQHSPISSDFAVKIRELDYLLQDYPVIVASN 63
OY 4 LAPAMSPYTLILLILLSSGLSTQDSFQHSPISSDFAVKIRELDYLLQDYPVIVASN 63
DB 401 LPPAPADELY-----SPITGE-----KIPASK 424
DB 401 LPPAPADELY-----SPITGE-----KIPASK 424
OY 64 LQDEELCGGLMRLVLAQRME-RLKTV-----AGSKMGLLENVNTEIHF 107
OY 64 LQDEELCGGLMRLVLAQRME-RLKTV-----AGSKMGLLENVNTEIHF 107
DB 425 MOEHNRIG-----LLDRRWLEQRDRSIRERQSDDEVAPGLDISSILKQLAER-RDIDFG 478
DB 425 MOEHNRIG-----LLDRRWLEQRDRSIRERQSDDEVAPGLDISSILKQLAER-RDIDFG 478
OY 108 VTKCA-----FQPPPSCLRF-----VQNNISRLQOETSEQLVALKPMI 145
OY 108 VTKCA-----FQPPPSCLRF-----VQNNISRLQOETSEQLVALKPMI 145
DB 479 VEEFAIKKIGEEIOQPEEKVYWDHSGSMARTQAQAQNTI--LOEOLEAIHKAKGLV 536
DB 479 VEEFAIKKIGEEIOQPEEKVYWDHSGSMARTQAQAQNTI--LOEOLEAIHKAKGLV 536
OY 146 -----SRCTLEOCOP-----DSSTLP-----PPWSRPLEAT-----APT 180
OY 146 -----SRCTLEOCOP-----DSSTLP-----PPWSRPLEAT-----APT 180
DB 537 PEDTKEKIGSKPNEIPQDPPPPSSATNIPSSAPITTSVPRPTMPPTVIVSAVPV 536
DB 537 PEDTKEKIGSKPNEIPQDPPPPSSATNIPSSAPITTSVPRPTMPPTVIVSAVPV 536

RESULT 7
ID TNR3_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lymphotoxin-beta receptor precursor.
GN ITRR OR TNFR3 OR TNFRSF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=Lung;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.,
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
RT and expression.";
RL J. Immunol. 155:5280-5288(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakamura T., Tashiro K., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL; U29173; AAA68964.1; -
DR EMBL; L38423; AB00846.1; -
DR EMBL; U30798; AA81334.1; -
DR HSSP; P25942; 1CDF.
DR MGD; MGI:104875; Ltbr.
DR InterPro: IPR001363; TNFR_C6.
DR Pfam; PF000771; TNFR_C6; 1.
DR PRODOM; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT REPEAT 42 81 CYTOPLASMIC (POTENTIAL).
FT REPEAT 82 124 TNFR-CYS 1.
FT REPEAT 125 170 TNFR-CYS 2.
FT REPEAT 171 213 TNFR-CYS 3.
FT REPEAT 214 258 TNFR-CYS 4.
FT DISULFID 43 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.

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FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 415;
 Best Local Similarity 24.4%; Pred. No. 3.3;
 Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAPPPSCL-----RPV-----QINISRLQETSEQLVAKPWITRONFS 151
 DB 123 ECRCPGMSGVILNDCVACEBERLVLCQPGTEAEVDEIMDTVNCVCKRGHONTSS 182
 QY 152 RCLLECCPDSSSTLPPEWSPRLEATAP-----TAPQPLLLLLLPVGLL--- 198
 DB 183 P-RANCOHTHC-----EIOGLVEARPOTSYSIDTCKNPPPGAMLLALISLVFL 235
 QY 199 ----IAANCLMQRTR-----RTPPPGCVPPVSPQ 228
 DB 236 FTVTLACAMMRHPSLCRKLGLTLKRHP-GEESPCCAPR 274

RESULT 8
 MRIP_DROME STANDARD; PRT; 479 AA.
 AC P20483; Q9VAL9;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE M-phase inducer phosphatase (EC 3.1.3.48) (String protein) (Cdc25-1-like protein).
 GN SFG OR CDC25 OR CG1395.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=69195217; PubMed=2702688;
 RA Edgar B.A., O'Farrell P.H.;
 RT "Genetic control of cell division patterns in the Drosophila embryo."
 RL Cell 57:177-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9106056; PubMed=2120044;
 RA Jimenez J., Alphey L., Nurse P., Glover D.M.;
 RT "Complementation of fission yeast cdc2ts and cdc2ts mutants
 RT identifies two cell cycle genes from Drosophila: a cdc2 homologue and
 RT string".
 RL EMBO J. 9:3565-3571(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champé M., Pfeiffer B.D.,
 RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale U., Bayraktaroglu L., Beaskey E.M.,
 RA Beeson K.Y., Benos P.V., Bernan E.P., Bhandari D., Bolshakov S.,
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gebhart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegan C.,
 RA Jaitli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maltel B., McIntosh T.C., Moledor M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Moritz J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacile J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
 CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE REQUIRED FOR
 CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
 CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O - protein
 CC tyrosine + phosphate.
 CC -!- SIMILARITY: STROGNE. TO OTHER SPECIES M-PHASE INDUCER PHOSPHATASE
 CC AND IN GENERAL TO PROTEIN-TYROSINE PHOSPHATASES.
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 CC CC
 CC EMBL: M24909; AAA28916.1; -;
 CC EMBL: X57495; CAA40732.1; -;
 CC EMBL: AE003768; AAF56885.1; -;
 CC PIR: A32290; A32290.
 CC PIR: S12008; S12008.
 CC HSSP: P30305; 10B0.
 CC Flybase; FBgn0003525; stg.
 CC InterPro; IPR000751; MPI_Phosphatase.
 CC InterPro; IPR001763; Rhodanese_domain.
 CC Pfam; PF00581; Rhodanese.
 CC PRINTS; PR00716; MPEPHATASE.
 CC SMART; SM00450; RHOD; 1.
 CC Cell division; Mitosis; Hydrolyase.
 CC ACT_SITE 379 379 BY SIMILARITY.
 CC CONFLICT 228 228 A -> T (IN REF. 1).
 FT SEQUENCE 479 AA; 54094 MW; 68483F3A2A58962CC CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 479;
 Best Local Similarity 22.9%; Pred. No. 3.8;
 Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;
 OY 1 MYVIAWMSPTTYLT-----LLLSGLSGTQDCPSFQSPISDFAVKTRFSDYLLDYP 57
 DB 72 MGLSPGSGSPQRQVLRQKILPAMGVSS-----DHPFAPS-FRI-FNSLSS-----T 117
 OY 58 VIVASNLQDEBLQGLWRLVLAQRMMERIKTVYAGSKMGLLEIRVNTFHEVTKCAFQPPP 117
 DB 118 CSWSSMDDE-----YMELEFMSQSQ-----QTAIGF-----P 146

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OY 118 SCLRPVOTNISRLOETSEQLVAKP---WITRONFSCLEL-QCQPDSSSTLPSPSPR 173
DB 147 SGLN-----SLISQIQEOPAKSPAGLSMRPSVRCISLMTSTNTSTTPPKTPE- 199
OY 174 LEATAPFA---POPPLLLLLLPVGLLLAAMCLHMORTRRRTPRGEQVPVPSPDPL 230
DB 200 ---TARDCFKRPEPP-----ASANCSPIOSKRHRCAAAVEKENCAPAPLSQ 242
OY 231 LVEH 235
DB 243 VTISH 247

RESULT 9
DRL_RAT STANDARD: PRT; 910 AA.
AC 063474;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
DE (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
DE DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
DE PTK-3).
GN DRL1 OR EDDR1 OR PTK3.
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RA MEDLINE=94173920; PubMed=8127887;
RT Sanchez M.P., Tapley P., Saini S.S., He B., Pulido D., Barbacid M.;
RT "Multiple tyrosine protein kinases in rat hippocampal neurons:
RT Isolation of Ptk-3, a receptor expressed in proliferative zones of
RT the developing brain.";
RT Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
RL
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO
CC PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
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CC -----
CC EMBL; L26525; AAA21089.1; -.
CC HSSP; P11362; IAGW.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR000421; FAS6_C.
CC InterPro: IPR002011; Receptor_tyr_kin_II.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00754; F5_F8_Type_C; 1.
CC Pfam: PF00069; pkinase; 1.
CC SMART; SM00231; FA58C; 1.
CC SMART; SM00219; TYRC; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
CC PROSITE; PS01285; FA58C_1; 1.

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DR PROSITE; PS01286; FA58C_2; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Tyrosine-protein kinase; Glycoprotein; Signal;
KW Phosphorylation; Transmembrane; Receptor; ATP-binding.
FT SIGNAL 1 19
FT CHAIN 20 910
FT DOMAIN 20 413
FT TRANSMEM 414 440
FT DOMAIN 441 910
FT DOMAIN 32 186
FT FT
FT DOMAIN 378 412
FT DOMAIN 473 598
FT DOMAIN 607 902
FT NP_BIND 613 621
FT BINDING 652 652
FT ACT_SITE 763 763
FT DISULFID 32 186
FT MOD_RES 510 510
FT MOD_RES 789 789
FT MOD_RES 793 793
FT MOD_RES 794 794
FT CARBOHYD 212 212
FT CARBOHYD 261 261
FT CARBOHYD 371 371
FT CARBOHYD 391 391
FT SEQUENCE 910 AA; 101164 MW; 7E7FFA1DCB029806 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 910;
Best Local Similarity 24.5%; Pred. No. 8.8; Mismatches 35; Indels 70; Gaps 9;
Matches 38; Conservative 12;

OY 143 PWITRONFSCLELOCQPDSTLP-PW---SPRPLEATA---PTAPDP----- 184
DB 356 PWLFSLSLTSIDV-VNDSDFPPAPWMPGPPTTFSSLELEPGQGVAKAEGSPFA 414
OY 185 -----PLLLLLLLPVGLLLAAMCLHMOR-----TRRR-----T 214
DB 415 ILICGLVAIIILLILLIALLML---WRLHMRLLSKRAERVLSEELTVHLSPGDTITLIN 470
OY 215 PRGEQVPP-----VPSQDPLL 232
DB 471 NRPGPREPPYQERPPACTPTPHAPCPVNSALL 505

RESULT 10
DRL_MOUSE STANDARD: PRT; 911 AA.
ID DRL_MOUSE
AC 003146;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
DE (Tyrosine-protein kinase CAK) (Cell adhesion kinase) (Tyrosine kinase
DE DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
DE MPK-6).
GN DRL1 OR EDDR1 OR CAK OR MPK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL;
RX MEDLINE=96204002; PubMed=8622863;
RA Perez J.L., Jing S.Q., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
RT coexpressed in breast tumor cell lines.";
RT Oncogene 12:1469-1477(1996).
RL
RN [2]
RN SEQUENCE OF 766-822 FROM N.A.
RP STRAIN=C57BL; TISSUE=Embryonic brain;
RC

```


RA Emerson P.C., Billinton A., Marshall F.H.;
 RT "The GABAB receptor interacts directly with the related transcription
 RT factors CREB2 and ATFx.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13967-13972(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kohraki J., Tanaka K.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 161-282 FROM N.A.
 RX MEDLINE-99303793; PubMed-10373550;
 RA Patl D., Melstreich M.L., Plon S.E.;
 RT "Human Cdc34 and Rad6b ubiquitin-conjugating enzymes target repressors
 RT of cyclic AMP-induced transcription for proteolysis.";
 RL Mol. Cell. Biol. 19:5001-5013(1999).
 CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)
 CC (CONSENSUS: 5'GTGAGCT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY
 CC VIRAL AND CELLULAR PROMOTERS.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER (POTENTIAL). INTERACTS WITH GABAB
 CC RECEPTOR.
 CC -1- SIMILARITY: TO OTHER BZIP PROTEINS.
 CC -----
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 CC -----
 DR EMBL; AF305687; AAG22558.1; -;
 DR EMBL; AB021663; BAA78477.2; -;
 DR EMBL; AF101368; AAD28370.1; -;
 DR MIM; 606398; -;
 DR InterPro: IPR002637; HamP-like.
 DR InterPro: IPR001871; bZIP.
 DR Pfam: PF00170; bZIP.1.
 DR ProDom: PD004952; HamP-like.1.
 DR SMART: SM00338; BRLZ.1.
 DR PROSITE; PS00036; BZIP_BASIC.1.
 DR Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Multigene family.
 FT DOMAIN 123 139 POLY-PRO.
 FT DOMAIN 186 194 POLY-PRO.
 FT DNA_BIND 210 230 BASIC MOTIF.
 FT DOMAIN 236 250 LEUCINE-ZIPPER (PROBABLE).
 FT COMPLECT 161 163 LIR->RHR (IN REF.3).
 FT SEQUENCE 282 AA; 30674 MW; DDB2P907CA0215A0 CRC64;

Query Match 6.8%; Score 85; DB 1; Length 282;
 Best Local Similarity 29.9%; Pred. No. 3.4;
 Matches 38; Conservative 7; Mismatches 38; Indels 44; Gaps 6;

QY 14 WIT-RQNSRQLEIQCPDSSITLPPSPSP--LEATA----- 178
 DB 66 WTEKVDSTALPLPLPPLPPTLPQP-SPHPDLEAASLKLKELROMEDFLDAPLPP 124
 QY 179 ---PTAPQPLLILLPLVGV-----LLAAMCLH--WORTRRTPPGSQ 220
 DB 125 PSPPLPPLPPLPAPSLPLSPFDLQPPVLDLTLALTYCENAGQEVGMPFLPQPQ 184
 QY 221 VPPVPS 227
 DB 185 QPPPPSP 191

RESULT 14
 FCQN_RAT STANDARD; PRT; 366 AA.
 AC P13599;
 DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE IGG receptor FCNRL large subunit p51 precursor (FCNRL) (Neonatal FC
 DE receptor) (IGG FC fragment receptor transporter, alpha chain).
 GN FCGR1 OR FCNRL.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OK NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX STRAIN-WISTAR;
 FC MEDLINE-89097257; PubMed-2911353;
 RA Simister N.E., Mostov K.E.;
 RT "An Fc receptor structurally related to MHC class I antigens.";
 RL Nature 337:184-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Epithelium;
 RX MEDLINE-90315866; PubMed-2534798;
 RA Simister N.E., Mostov K.E.;
 RT "Cloning and expression of the neonatal rat intestinal Fc receptor, a
 RL major histocompatibility complex class I antigen homolog.";
 RN Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-95059482; PubMed-7969498;
 RA Burneister W.P., Huber A.H., Bjorkman P.J.;
 RT "Crystal structure of the complex of rat neonatal Fc receptor with
 RT Fc.";
 RL Nature 372:379-383(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-98154319; PubMed-9493268;
 RA Vaughn D.E., Bjorkman P.J.;
 RT "Structural basis of pH-dependent antibody binding by the neonatal Fc
 RT receptor.";
 RL Structure 6:63-73(1998).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
 CC NEWBORN ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
 CC RESULTANT FCNRL-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCNRL INTO BLOOD OR
 CC TISSUE FLUIDS (BY SIMILARITY).
 CC -1- SUBUNIT: FCNRL COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
 CC LIKE HETERODIMER.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -----
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 CC -----
 DR EMBL; X14323; CAA32503.1; -;
 DR EMBL; M35495; AAA41611.1; -;
 DR PIR; S02117; S02117.
 DR PIR; A37374; A37374.
 DR PDB; 1FRT; 14-FEB-95.
 DR PDB; 3FRT; 10-JUN-98.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam; PF00047; Ig_1.
 DR Pfam; PF00129; MHC_I_1.
 DR ProDom; PD000050; MHC_I_1.
 DR SMART; SM00407; IgG1; 1.

DR PROSITE: PS00230; IG_MHC. 1.
 KW IG-binding protein; Receptor; Transmembrane; Glycoprotein; signal;
 KM Immunoglobulin domain, 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 366
 FT DOMAIN 23 111
 FT DOMAIN 112 201
 FT DOMAIN 202 291
 FT DOMAIN 292 322
 FT DOMAIN 323 366
 FT DISULFID 120 183
 FT DISULFID 222 276
 FT CARBOHYD 109 109
 FT CARBOHYD 126 126
 FT CARBOHYD 150 150
 FT CARBOHYD 247 247
 SQ SEQUENCE 366 AA; 40168 MW; 8A8BF2873A698B5 CRC64;
 Query Match 6.8%; Score 85; DB 1; Length 366;
 Best Local Similarity 22.2%; Pred. No. 4.6;
 Matches 51; Conservative 21; Mismatches 66; Indels 92; Gaps 11;
 OY 46 RELSDYLLQDPYVAVASNLQDEELCGIMRLVLAORME---RLKTVAGSKMGGLEHY 101
 DB 173 RKESEFLITSCP-----ERLGLHLEGRONLEMKRPPSRMLKARONGSSVYL--- 220
 OY 102 NTEIHEVTKCA---FQPPSCLPFVQTNISRLQETSEDLVALKPWITQNFNSRC----- 153
 DB 221 -----TCAAFSFYPPELKFRLRNGLA-----SGSGNCSSTGPN 253
 OY 154 -----LEL-----OCOPDSRLPPMSPRELPAPAPAPAPPLLLLPYG 195
 DB 254 GDGSFHAMSLLEPKRGDEHHYOCQVEHGLAQLT---VDLSPASSVPVGGIIL---G 307
 OY 196 LLLLA---AANCLHMOTRRRTPR-----FQEOVPVPSQ 228
 DB 308 LLLVVAAGVLLMNMRRSGLPAPWLSGDSDGLLPGNLLPPEAPEQ 357
 RESULT 15
 ABFL_MOUSE
 ID ABFL_MOUSE STANDARD; PRT; 3726 AA.
 AC Q61329;
 DT 16-OCT-2001 (Rel. 4.0, Created)
 DT 16-OCT-2001 (Rel. 4.0, Last sequence update)
 DT 16-OCT-2001 (Rel. 4.0, Last annotation update)
 DE Alpha-fetoprotein enhancer binding protein (AT motif-binding factor)
 DE (AT-binding transcription factor).
 GN AFPFL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/MK X ICR; TISSUE=Brain;
 RX MEDLINE=96194902; PubMed=8654949;
 RA Ito A., Miura Y., Watanabe M., Sakai M., Inoue Y., Miki T.,
 RA Hashimoto T., Morinaga T., Nishi S., Tamaki T.;
 RT "Cloning of the cDNA encoding the mouse Abfl transcription factor.";
 RL Gene 168:227-231(1996).
 CC -1- FUNCTION: Transcriptional activator that binds to the AT-rich core
 CC sequence of the enhancer element of the AFP gene.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: CONTAINS 4 HOMEBOX DOMAINS.
 CC -----
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 CC -----
 CC EMBL: D26046; BAA05046.1; -
 DR HSSP; P06601; IEJL.
 DR MGD; MGI:99948; Abfl.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR003604; Znf.U1.
 DR InterPro; IPR000822; Znf.C2H2.
 DR Pfam; PF00046; homeobox.4.
 DR Pfam; PF00096; zfc2h2; 20.
 DR SMART; SM00389; HOX; 4.
 DR SMART; SM00355; Znf.C2H2; 22.
 DR SMART; SM00451; Znf.U1; 7.
 DR PROSITE; PS00027; HOMEBOX_1; 2.
 DR PROSITE; PS00071; HOMEBOX_2; 4.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 9.
 KW Transcription regulation; Activator; Zinc-finger; Metal-binding;
 KM DNA-binding; Homeobox; Nuclear protein; Repeat.
 FT ZN_FING 79 103
 FT ZN_FING 282 305
 FT ZN_FING 641 664
 FT ZN_FING 672 695
 FT ZN_FING 727 751
 FT ZN_FING 805 829
 FT ZN_FING 946 969
 FT ZN_FING 985 1009
 FT ZN_FING 1041 1065
 FT ZN_FING 1089 1113
 FT ZN_FING 1233 1256
 FT ZN_FING 1262 1285
 FT ZN_FING 1370 1395
 FT ZN_FING 1411 1433
 FT ZN_FING 1439 1462
 FT ZN_FING 1555 1579
 FT ZN_FING 1606 1630
 FT ZN_FING 1690 2013
 FT ZN_FING 2152 2211
 FT DNA_BIND 2249 2308
 FT ZN_FING 2335 2358
 FT ZN_FING 2539 2561
 FT DNA_BIND 2650 2709
 FT ZN_FING 2720 2743
 FT DNA_BIND 2952 3011
 FT ZN_FING 3032 3056
 FT ZN_FING 3552 3576
 FT DOMAIN 461 491
 FT DOMAIN 771 785
 FT DOMAIN 1314 1317
 FT DOMAIN 1734 1748
 FT DOMAIN 1794 1799
 FT DOMAIN 1856 1863
 FT DOMAIN 2044 2059
 FT DOMAIN 2405 2408
 FT DOMAIN 3216 3220
 FT DOMAIN 3380 3409
 FT DOMAIN 3412 3420
 FT DOMAIN 3534 3550
 FT DOMAIN 3620 3623
 FT DOMAIN 3659 3662
 SQ SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;
 Query Match 6.8%; Score 84.5; DB 1; Length 3726;
 Best Local Similarity 21.6%; Pred. No. 71;
 Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;
 OY 29 DCSFQHSPISSDAVKITRELSYLLQDPYVAVASNLQDEE--LCCGLMRLVLAORMERL 86
 DB 3033 ECTLGKIKYARLSRDLHSQOHISKVKDITGSOILDKKEKFEFPAVYKOLMAQOQELDR 3092
 OY 87 KTV-----ASGKMGGL-----LERVNTETIHEVTKAFQ--PP-----PSCLEFVQTN 126

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Db 3093 KKANVGLAAQQGFMNAPLQALNLP---TTPPALGIPVLLPGLNRSPLPGFTPAN 3149
QY 127 ISRLQETSEQLVAKPWITRONFSRCLQCCQPSSTLPPW-----S 170
Db 3150 TA-----LTSKPR-----NLMLP-STYVSPGCLPTSGLPKPKSSASLSS 3188
QY 171 PRELEATAPAPAPPLLLLLLPLVGLLLLAAMCLHMORTRRTPRPEEQVP----- 223
Db 3189 PTPAQATMAAPQPP-----PQOPQOPPPVQOPPPPPAAQQ 3224
QY 224 VPSPQ 228
Db 3225 IPAPQ 3229

RESULT 16
MNT_HUMAN STANDARD: PRT; 582 AA.
AC 099583;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE MAX binding protein MNT (ROX protein) (MYC antagonist MNT).
GN MNT OR ROX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=97327566; PubMed=9184233;
RA Meroni G., Raymond A., Alcalay M., Borsani G., Tanigami A.,
RA Tonlorenzi R., Lo Nigro C., Messali S., Zollo M., Ledbetter D.H.,
RA Brent R., Ballabio A., Carrozzo R.;
RT "Rox, a novel bHLHZip protein expressed in quiescent cells that
RT heterodimerizes with Max, binds a non-canonical E box and acts as a
RT transcriptional repressor.";
RL EMO J. 16:2892-2906(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98260677; PubMed=9598315;
RA Nigro C.L., Venesio T., Raymond A., Meroni G., Alberici P.,
RA Calanca S., Enrico F., Stack M., Ledbetter D.H., Lisica D.S.,
RA Ballabio A., Carrozzo R.;
RT "The human ROX gene: genomic structure and mutation analysis in human
RT breast tumors.";
RL Genomics 49:275-282(1998).
CC -1- FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES
CC TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE
CC 5'-CAGCG-3' AND, WITH HIGHER AFFINITY, TO 5'-CAGCG-3'.
CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
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CC
DR EMBL: X96401; CAA65265.1; -
DR EMBL: Y13440; CAA73851.1; -
DR EMBL: Y13441; CAA73851.1; JOINED.
DR EMBL: Y13442; CAA73851.1; JOINED.
DR EMBL: Y13443; CAA73851.1; JOINED.
DR EMBL: Y13444; CAA73851.1; JOINED.
DR HSSP: P25912; IHL0.

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DR TRANSFAC; T03268; -.
DR MIM: 603039; -.
DR InterPro: IPR003015; HLH_Myc.
DR InterPro: IPR001092; HLH_dim.
DR Pfam: PF00010; HLH_1.
DR SMART: SM00353; HLH_1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; FALSE_NEG.
KW Transcription regulation; Repressor; Nuclear protein; DNA-binding.
FT DNA_BIND 222 233 BASIC DOMAIN.
FT DOMAIN 234 270 HELIX-LOOP-HELIX MOTIF (POTENTIAL).
FT DOMAIN 271 299 LEUCINE-ZIPPER.
SQ SEQUENCE 582 AA; 62299 MW; 06AC320D79BF18A0 CRC64;

Query Match 6.8%; Score 84; DB 1; Length 582;
Best Local Similarity 21.1%; Pred. No. 9.4;
Matches 61; Conservative 35; Mismatches 89; Indels 104; Gaps 13;

QY 4 LAPASPTTYLLLLLLLS-----GLSOTDSCFQHSPISSDPAVKITRELSDY 51
Db 186 LAPQPPPTLTGLKLAPEVYKSEQKKRPGIGTRV---HNKLEKNRAHLKEGEET 242
QY 52 LLDYPTVYASMLQDEELCGIMRLVLAORMMERIKTVAGSKQGLLERVNTEHFTYKC 111
Db 243 LKENIP-----NVDDKK-TSNLSVLTALRYIQSLKR-KEKEYHEMERLARE-----KI 290
QY 112 APQPPRSCLRFVQNTISRLQETSEQLVAKPWITRONFSRCLQCCQPD----- 161
Db 291 A-----TQRLAEKLHELSC-----WMDVEIDRYLQGTQGPEDDQASTSTAS 333
QY 162 -----STLPP-WSPRELEATAPAPQPLLLL 189
Db 334 EGEDNIDEMEDRAGLGPRLSHRPOPELLKSTLPPSTTPADL---PPHPRH---- 385
QY 190 LLLPVGLLLLAAMCLHMORTRRTPRPEEQVP-----VPSPQDL 231
Db 386 ---PNSVALPRHLVYQQQPGQKTRLPAPPPPPAAGTIVPRAHLY 431

RESULT 17
YF48_HUMAN STANDARD: PRT; 732 AA.
AC 09HCW4; Q9H975;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA1548.
GN KIAA1548.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunawa H., Ishii S., Kawai I., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahara K., Masuho Y., Sasaki N.;
RT "NEO human cDNA sequencing project.";
RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 188-732 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:237-261(2000).
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
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RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
CC -1 FUNCTION: COMPONENT OF THE SARCOGLYCIN COMPLEX, A SUBCOMPLEX OF
CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE
CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. SARCOLEMMAL
CC (POTENTIAL).
CC -1 SIMILARITY: BELONGS TO THE SARCOGLYCIN ALPHA/EPSILON FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB024920; BAA83491.1; -
DR EMBL: AF064081; AAC33447.1; -
DR MGD: MGI:894698; Sgca.
RM Cytoskeleton; Transmembrane; Glycoprotein; Signal.
FM SIGNAL 1 23
FM CHAIN 24 387
FM DOMAIN 24 293 EXTRACELLULAR (POTENTIAL).
FM TRANSMEM 294 314 POTENTIAL.
FM DOMAIN 315 387 CYTOPLASMIC (POTENTIAL).
FM CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FM CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 387 AA; 43286 MW; 7C3D98A853D04591 CRC64;

Query Match 6.5%; Score 81; DB 1; Length 387;
Best Local Similarity 22.7%; Pred. No. 11;
Matches 69; Conservative 26; Mismatches 99; Indels 110; Gaps 14;

OY 11 TTYVLLLLLSGLSGTODCSFQHSPISSDFAKIRLESDYLDQPYTVASNDDELC 70
DB 115 TTRORLLLTG-----DEGRPLRYOAEFLRSHDEEVL-----PTTPANRL--TAL 161
OY 71 GGLN-----RLVLAQRMERLKTVAASKMOGLLERYNEIHFVT-----K 110
DB 162 GGLMEPELQDLNITSALDRGGRVPLRIGRKEGYIKVGSATPSTCLKWASPSYAR 221
OY 111 CAFQRP--SC-----LRFVQTNISRLQETSBDYALKWITRQFSCLEACOPD 161
DB 222 CAGQGFPLSCYDTLAPHFVWMCNVLVDKSVPELD-----EVLTPGD 266
OY 162 SSTLPWPSPRLPAA-----APYAPQRPVLLLLLPVGLLLAAMC----- 204
DB 267 GILHDPFPCPTEADRDQFLDALVTLLVPLVALL--TLLATYMCRRREGRLKRD 323
OY 205 -----LHMQRTRRRTPRP-----GEQVPR-VPSPO-DL 231
DB 324 MATSDIQMFHHSIHGNTETELROMASREVPRPLSTLPMFNVRIGERLPRVDSQMPLI 383
OY 232 LVEH 235
DB 384 LDOH 387

RESULT 25
RQC_HUMAN STANDARD; PRT; 428 AA.
AC P01854;
DR 21-JUL-1986 (rel. 01, Created)
DR 21-JUL-1986 (rel. 01, Last sequence update)
DR 16-OCT-2001 (rel. 40, Last annotation update)
DE Ig epsilon chain C region.
GN IGHE
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=83168897; PubMed=6300763;
RA Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igatahi K.,
RA Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
RT "Molecular cloning and nucleotide sequencing of human immunoglobulin
RT epsilon chain cDNA."
RL Nucleic Acids Res. 11:719-726(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83001945; PubMed=6288268;
RA Max E.E., Bailey U., Ney R., Kirsch I.R., Leder P.;
RT "Duplication and deletion in the human immunoglobulin epsilon genes."
RL Cell 29:691-699(1982).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236029; PubMed=6234164;
RA Flanagan J.G., Rabbits T.H.;
RT "The sequence of a human immunoglobulin epsilon heavy chain constant
RT region gene and evidence for three non-allelic genes."
RL EMBO J. 1:655-660(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84207910; PubMed=6327276;
RA Ueda S., Nakai S., Nishida Y., Hiseajima H., Honjo T.;
RT "Long terminal repeat-like elements flank a human immunoglobulin
RT epsilon pseudogene that lacks introns."
RL EMBO J. 1:1539-1544(1982).
RN [5]
RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
RA Benlich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RT Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
RN [6]
RP SEQUENCE OF 1-40: 68-114 AND 427-428 FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Moigard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line."
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [7]
RP 3D-STRUCTURE MODELING.
RA Padlan E.A., Davies D.R.;
RL "A model of the Fc- of immunoglobulin E."
RL Submitted (JUL-1993) to the PDB data bank.
CC -----
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CC -----
DR EMBL: L00022; AAB59424.1; ALU_INT7.
DR PIR: A02142; EHHU.
DR PIR: A22771; A22771.
DR PIR: A23195; A23195.
DR PDB: 1IGE; 15-JUL-92.
DR MIM: 147180; -
DR InterPro: IP0003006; Ig_MHC.
DR InterPro: IP0003597; Ig_c1.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00407; Ig_c1; 4.
DR PROSITE: PS00290; IG_MHC; 3.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 15 105
FT DISULFID 29 85
FT DISULFID 121 121 INTERCHAIN (WITH A HEAVY CHAIN).

```


FT	DISULFID	135	193	
FT	DISULFID	209	209	
FT	DISULFID	239	299	
FT	DISULFID	345	405	
FT	CARBOHYD	21	21	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	146	146	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	252	252	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	275	275	N-LINKED (GLCNAC. . .)
FT	VARIANT	359	359	W -> L (IN REF. 2, POSSIBLY DUE TO POLYMORPHISM).

INTERCHAIN (WITH A HEAVY CHAIN).

SEQUENCE 428 AA; 47019 MW; 25C4CA072AA558A0 CRC64; /FTIG-VAR_003885.

Query Match Best Local Similarity 6.5%; Score 81; DB 1; Length 428;

Matches 48; Conservative 21; Mismatches 83; Indels 70; Gaps 8;

QY	2	TVLAPANSPTT---	YLILLSSGLSGTQ--DCSFQHSPISSDF-----	41
Db	52	TMTLPATTLTSLGHTATISLITVSGAMAKQMFRCRAVAHPPSTDMVDNKTFSVCSRDFTF	111	
QY	42	-----	AVKIRELSDYLDQDPYTVASNLQDEEL	69
Db	112	PTVKIIQSCDGGGHEPPIQLCLVSGYTPGTINITWLEDQVMDVDLSTASTQEGEL	171	
QY	70	CGGLMRVLVAQR-WMERLKTVAGSKMGLERVNTIEHFVTKCAFQPPPCLEFVQTNIS	128	
Db	172	ASTQSELTLSOKHWSRRTYTCQVYQGHTEFEDSTK-----KCADSNP-----RGYSAYIS	222	
QY	129	RLLOETSEQLVALKFWTTTRQNFRCLELQCPDSSSTLPPPWS	170	
Db	223	R-PSPPDLFIRKSPIT-----CLVVDLAPSKGTVNLTWS	256	

Search completed: August 6, 2002, 09:46:19
Job time: 400 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:39:04 ; Search time 47.12 Seconds

(Without alignments)
862.772 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242
Sequence: 1 MTVLAPAMSPRTYLLILL.....RPEQVPPVSPDILLVH 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :
1: SP archaea:.*
2: SP bacteria:.*
3: SP fungi:.*
4: SP human:.*
5: SP invertebrate:.*
6: SP mammal:.*
7: SP mhc:.*
8: SP organelle:.*
9: SP phage:.*
10: SP plant:.*
11: SP rodent:.*
12: SP virus:.*
13: SP vertebrate:.*
14: SP unclassified:.*
15: SP virus:.*
16: SP bacteriophage:.*
17: SP archaea:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895.5	72.1	294	6 Q9MZV0	Q9MZV0 canis fam1
2	894.5	72.0	291	6 Q9MZV0	Q9MZV0 felis silve
3	840	67.6	292	6 Q9GKE0	Q9GKE0 bos taurus
4	746	60.1	274	6 Q9GKE0	Q9GKE0 bos taurus
5	602.5	48.5	172	11 Q61104	Q61104 mus musculu
6	112.5	9.1	579	10 Q9LGS8	Q9LGS8 oryza sativ
7	104.5	8.4	668	5 Q9GY11	Q9GY11 leishmania
8	102.5	8.3	648	5 Q9GY33	Q9GY33 leishmania
9	98.5	7.9	345	5 Q9N753	Q9N753 leishmania
10	95.5	7.7	1240	12 Q9DWH8	Q9DWH8 rat cytochrome
11	93.5	7.5	658	10 Q9C5F0	Q9C5F0 arabidopsis
12	93	7.5	1217	5 Q17889	Q17889 caenorhabdi
13	92.5	7.4	560	5 Q9GY11	Q9GY11 leishmania
14	92	7.4	560	5 Q9HAD2	Q9HAD2 homo sapien
15	90.5	7.3	536	5 Q9GYA0	Q9GYA0 leishmania
16	90.5	7.3	660	5 Q9GY15	Q9GY15 leishmania

17	90.5	7.3	5120	13 Q9PU36	Q9PU36 gallus gall
18	89.5	7.2	474	5 Q17610	Q17610 caenorhabdi
19	88.5	7.1	270	4 Q9DWT1	Q9DWT1 homo sapien
20	88.5	7.1	404	10 Q9AMJ4	Q9AMJ4 oryza sativ
21	88.5	7.1	1267	10 Q943D5	Q943D5 oryza sativ
22	88.5	7.1	1386	4 Q75064	Q75064 homo sapien
23	88	7.1	250	6 Q9GKE2	Q9GKE2 sus scrofa
24	88	7.1	675	11 Q9DBT2	Q9DBT2 mus musculu
25	88	7.1	733	12 Q56971	Q56971 kenedya ye
26	87.5	7.0	470	10 Q9JUI1	Q9JUI1 arabidopsis
27	87.5	7.0	946	10 Q22015	Q22015 cyllindroche
28	87	7.0	510	5 Q44018	Q44018 leishmania
29	86.5	7.0	299	6 Q9TTF9	Q9TTF9 bos taurus
30	86	6.9	255	11 Q9D3J3	Q9D3J3 mus musculu
31	86	6.9	299	12 Q84647	Q84647 paramecium
32	86	6.9	706	5 Q23600	Q23600 caenorhabdi
33	86	6.9	911	11 Q35407	Q35407 mus musculu
34	85.5	6.9	795	5 Q95U02	Q95U02 toxoplasma
35	85	6.8	282	4 Q9BSA1	Q9BSA1 homo sapien
36	85	6.8	289	16 Q9A3K1	Q9A3K1 caulobacter
37	85	6.8	413	11 Q99MM1	Q99MM1 mus musculu
38	85	6.8	1217	4 Q9P2D0	Q9P2D0 homo sapien
39	84.5	6.8	780	13 Q90X41	Q90X41 brachydanio
40	84.5	6.8	932	11 Q99JH4	Q99JH4 mus musculu
41	84.5	6.8	1134	4 Q96JH1	Q96JH1 homo sapien
42	84	6.8	220	4 Q96030	Q96030 homo sapien
43	84	6.8	224	6 Q19031	Q19031 ovis aries
44	84	6.8	263	12 Q36417	Q36417 alcelaphine
45	84	6.8	543	6 Q95NM2	Q95NM2 oryctolagus
46	84	6.8	567	11 Q99J43	Q99J43 mus musculu
47	84	6.8	1234	11 Q9R044	Q9R044 rattus norv
48	84	6.8	1252	11 Q9QX7	Q9QX7 rattus norv
49	84	6.8	1252	11 Q9JIX2	Q9JIX2 rattus norv
50	83.5	6.7	199	16 Q9RZL3	Q9RZL3 delnocoocus

ALIGNMENTS

RESULT	ID	Q9MZV0	PRELIMINARY;	PRT;	294 AA.
AC	Q9MZV0				
DT	01-OCT-2000	(TREMBlrel. 15, Created)			
DT	01-OCT-2000	(TREMBlrel. 15, Last sequence update)			
DT	01-OCT-2000	(TREMBlrel. 15, Last annotation update)			
DE	FLR3 LIGAND.				
OS	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
OX	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20358731; PubMed=10902925;				
RA	Yang S., Sim G.K.;				
RT	"Molecular cloning of canine and feline flt3 ligand reveals high				
RT	degree of similarity to the human and mouse homologue but uniquely				
RT	long cytoplasmic domain."				
RL	DNA Seq. 11:163-166(2000).				
DR	EMBL; AF15148; AAF87088.1; -				
SO	SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;				
Query Match 72.1%; Score 895.5; DB 6; Length 294;					
Best Local Similarity 77.1%; Pred. No. 7.9e-82;					
Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;					
QY	1	MTVLAPAMSPRTYLLILLSSGSGTQDSFQHSPTSSDFAKIRELSYLLQDPYVY	60		
DB	1	MTVLAPAMSPRTYLLILLSSGSGTQDSFQHSPTSSDFAKIRELSYLLQDPYVY	60		
QY	61	ASNDDELGGELRWLVLAORWMEKLVAGSKMGGLEEVNTEIHFWTCAPQPPSC	120		

Db 61 ASNLQDELGCAGFWRLVLAQRMWVRLQAVASQMOILLEAVNTEIHFTVFCAFQPLPSCL 120
 QY 121 RFVQNTISRLQETSQVLAQRMWVRLQAVASQMOILLEAVNTEIHFTVFCAFQPLPSCL 180
 RT 121 RFVQNTISRLQETSQVLAQRMWVRLQAVASQMOILLEAVNTEIHFTVFCAFQPLPSCL 180
 Db 121 RFVQNTISRLQETSQVLAQRMWVRLQAVASQMOILLEAVNTEIHFTVFCAFQPLPSCL 180
 QY 181 APQAPRLILLLLPVALLMSTAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 236
 Db 181 APQAPRLILLLLPVALLMSTAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 236

RESULT 2

Q9MKD9 PRELIMINARY; PRT; 291 AA.
 AC Q9MKD9; PRELIMINARY; PRT; 291 AA.
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE FLT3 LIGAND.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20358731; PubMed=10902925;
 RX Yang S., Sim G.K.;
 RT "Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain."
 RL DNA Seq. 11:163-166(2000).
 DR EMBL; AF15149; AAF87089.1; -
 SQ SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64;

Query Match

Best Local Similarity 72.0%; Score 894.5; DB 6; Length 291;
 Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 60
 RT 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 60
 Db 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 60
 QY 61 ASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 120
 RT 61 ASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 120
 Db 61 ASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 120
 QY 121 RFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 180
 RT 121 RFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 180
 Db 121 RFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 180
 QY 181 APQAPRLILLLLPVALLMSTAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 220
 RT 181 APQAPRLILLLLPVALLMSTAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 220
 Db 181 APQAPRLILLLLPVALLMSTAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 220

RESULT 3

Q9GKEO PRELIMINARY; PRT; 292 AA.
 AC Q9GKEO; PRELIMINARY; PRT; 292 AA.
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE FLT3 LIGAND ISOFORM-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20570936; PubMed=11120823;
 RX Mwangi W., Brown W.C., Palmer G.H.;

RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
 RT required for receptor binding and function using naturally occurring
 RT ligand isoforms."
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL; AF282985; AAF99322.1; -
 DR InterPro; IPR004213; flt3_1lg.
 DR Pfam; PF02947; flt3_1lg; 1.
 SQ SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match

Best Local Similarity 67.6%; Score 840; DB 6; Length 292;
 Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 59
 RT 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 59
 Db 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 59
 QY 60 VASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 119
 RT 60 VASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 119
 Db 60 VASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 119
 QY 120 LRFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 179
 RT 120 LRFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 179
 Db 120 LRFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 179
 QY 180 TAPQPP--LLLLLLLPVGLLLLAAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 220
 RT 180 TAPQPP--LLLLLLLPVGLLLLAAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 220
 Db 180 TAPQPP--LLLLLLLPVGLLLLAAMCLHWRRRRRRRSPYGEQRTLRPSRSHLPED 220

RESULT 4

Q9GKD9 PRELIMINARY; PRT; 274 AA.
 AC Q9GKD9; PRELIMINARY; PRT; 274 AA.
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE FLT3 LIGAND ISOFORM-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20570936; PubMed=11120823;
 RX Mwangi W., Brown W.C., Palmer G.H.;
 RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
 RT required for receptor binding and function using naturally occurring
 RT ligand isoforms."
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL; AF282985; AAF99323.1; -
 DR InterPro; IPR004213; flt3_1lg.
 DR Pfam; PF02947; flt3_1lg; 1.
 SQ SEQUENCE 274 AA; 30372 MW; 725A7F7A95DA98B CRC64;

Query Match

Best Local Similarity 60.1%; Score 746; DB 6; Length 274;
 Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;

QY 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 59
 RT 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 59
 Db 1 MTVLAPAMSPPT-LLLLLLLSGLSGTQDSCFQHSPISSDFAVKIRELSDYLLQDYPVT 59
 QY 60 VASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 119
 RT 60 VASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 119
 Db 60 VASNLQDELGCGLMRVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 119
 QY 120 LRFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 179
 RT 120 LRFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 179
 Db 120 LRFVQNTISRLQETSQVLAQRMWRLKTVAGSKQGLERVNTIEHFVTKCAFQPPSC 179


```
Db 149 LPPWSSMNPINQTLQVRLKLSGT-----LPADMS-SLKSLSNVLEDMPT----- 194
Qy 64 LQDEELCGGLMRVLAQRMMERLKTAVAGSKMGGLEERVNEIHVTCARQPP-----S 118
Db 195 -----GL-----LPPBW-----GSLERIQQLVLRKLTGTPLPQWSPMK 229
Qy 119 CLAREVO---TWISRLQ-----ETSEQLVALKP-WITRONFSRCLELQCP 160
Db 230 ALRRLTLDTGTLSTGLPQWMSAMASVISLNIEGTVEGTLPPKMSMSRL-QTLNLRRTK 288
Qy 161 DSSLTPPPWSPR-----PLEATAPAPQPP-----LILLILPVGLL--LLAAAV 203
Db 289 VSGTLPPWSSMGSILANLQSLTSGTLPQWSSMKRLQLTLTDLTLLSGTLPAEW 345

RESULT 8
Q9GY33 PRELIMINARY; PRT; 648 AA.
AC Q9GY33;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROBABLE SURFACE ANTIGEN P2.
GN LM12.121.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC02017.2; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR002965; P_rich_extensn.
DR Pfam; PF00560; LRR; 8.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00181; EGF_1.
SQ SEQUENCE 648 AA; 68470 MW; 8EB78AC101E01286 CRC64;

Query Match
Best Local Similarity 8.3%; Score 102.5; DB 5; Length 648;
Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

Qy 4 LAPWSPPTVYLLILLSSGISTGQDSFOHSPISDPAVKIRELSYLLQDYPVTYASN 63
Db 149 LPPWSSMNPINAVELKRLKLSGT-----LPADMS-SLKSLSNVLEDMPT----- 194
Qy 64 LQDEELCGGLMRVLAQRMMERLKTAVAGSKMGGLEERVNEIHVTCARQPP-----S 118
Db 195 -----GL-----LPPBW-----GSLERIQQLVLRKLTGTPLPQWSPMK 229
Qy 119 CLAREVO---TWISRLQ-----ETSEQLVALKP-WITRONFSRCLELQCP 160
Db 230 ALRRLTLDTGTLSTGLPQWMSAMASVISLNIEGTVEGTLPPKMSMSRL-QTLNLRRTK 288
Qy 161 DSSLTPPPWSPR-----PLEATAPAPQPP-----LILLILPVGLL--LLAAAV 203
Db 289 VSGTLPPWSSMGSILANLQSLTSGTLPQWSSMKRLQLTLTDLTLLSGTLPAEW 345

RESULT 9
Q9N753 PRELIMINARY; PRT; 345 AA.
AC Q9N753;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROBABLE SURFACE ANTIGEN P2.
```

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GN LM12.08.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAH98658.2; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00560; LRR; 3.
DR SMART; SM00370; LRR; 3.
SQ SEQUENCE 345 AA; 37530 MW; 06ECC850B1B54B70 CRC64;

Query Match
Best Local Similarity 7.9%; Score 98.5; DB 5; Length 345;
Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;

Qy 6 PAMSPPTVYLLILLSSGISTG-----QDCSFOHSPISDPAVKIRELS 49
Db 152 PEMGSMTSLSVINLRGTSGTLPQWSSMKSARSLQLODCLSGSLPSWSAI----- 205
Qy 50 DYLLQDYPVTYASNQDEELCG-----GLMRVLAQRMMERLKTAVAGSKMGGLEERVNTE 104
Db 206 -----PMLASVSLKGNKFCGVCCTRGIRRLVYL--WTSRSTRAATA----- 245
Qy 105 IHVTKCARQPP---PPSCLEEVQTNISRLQETSEQLVALKPWITRONFSRCLELQCP 161
Db 246 --WLRTAQRPPLSPPPRQRPRTSLT-----FPLRGRPR 278
Qy 162 SSTLPWSPRRLHATAPAPQPLLL-----LLPVGLLLAAACLMQRTTR 212
Db 279 LSRLPQALHRLN-----PPQPLHRLNPPPLP-----QOTRR 313

RESULT 10
Q9DWH8 PRELIMINARY; PRT; 1240 AA.
AC Q9DWH8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PR2.
GN R2.
OS Rat cytomegalovirus (strain Mastricht).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; MurinegaloVirus.
OX NCBI_TaxID=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RC MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome.";
RL J. Virol. 74:7656-7665(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RC MEDLINE=20473137; PubMed=11018281;
RA Gruijthuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
RT spliced transcript ";
RL Virus Res. 69:119-130(2000).
DR EMBL; AF232689; AAF99111.1; -.
SQ SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;

Query Match
Best Local Similarity 7.7%; Score 95.5; DB 12; Length 1240;
Matches 33; Conservative 10; Mismatches 57; Indels 101; Gaps 10;
```

Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;

QY 160 PDSSTL-----PPWSPRP--LEATAPAPQP-PLILLILPYGLILLAA 201
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 1060 PDSSTAVGATEATERSTPATEPRRYRPLPGVDSALPLAQPITLLILLVPA----- 1112

QY 202 AMCLHMQRTRRRPRGEGQVPPVPSPOD 229
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 1113 -----QATRASPRPETDAP-PTPAD 1132

RESULT 11
Q9G5T0 PRELIMINARY; PRT; 658 AA.

AC Q9G5T0; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
RE REEPOR-LIKE PROTEIN KINASE 4.
GN RIK4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20575726; PubMed=11135117;
RX Du L., Chen Z.;
RT "Identification of genes encoding receptor-like protein kinases as
RT possible targets of pathogen- and salicylic acid-induced WRKY DNA-
RT binding proteins in Arabidopsis.";
RL Plant J 24:837-847(2000);
DR EMBL; AF224705; AAK28315.1; -
DR InterPro: IPR002902; DUF26.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam; PF01657; DUF26; 2.
DR Pfam; PF00069; Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; kinase; transferase
SQ SEQUENCE 658 AA; 72991 MW; DCF9GCF5F1748F614 CRC64;

Query Match 7.5%; Score 93.5; DB 10; Length 658;
Best Local Similarity 25.8%; Pred. No. 0.72; Mismatches 39; Indels 43; Gaps 6;
Matches 34; Conservative 16;

QY 138 LVALKPWITRONFSRCLEL---QCQPD-----SSTLPPEWSPR 172
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 195 LVGCPDPLTRDQSCRCLQVLINQJPTDRIGARLIPSCSTSEYETIYAYTESAVPP--PP 252

QY 173 PLKATAPAPQP-----LILLILP--VGLILLAAACLHMQRTRRRPRP--- 217
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 253 PPSISTPEVSAPPRSEKSGSKVLVIAVPIVAVLFLAGYCFLLRAKSKYSTPSAF 312

QY 218 -GEOVPPVPSPO 228
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 313 AGDDITTTADSLQ 324

RESULT 12
O17889 PRELIMINARY; PRT; 1217 AA.

AC O17889; 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F54F12.1 PROTEIN.

GN F54F12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81548; CAB04464.1; -
DR HSSP; P18052; IYFO.
DR InterPro: IPR000387; TYR_phosphatase.
DR InterPro: IPR000242; Tyr_prot_phptase.
DR Pfam; PF00102; Y-phosphatase; 1.
DR SMART; SM00194; PTPc; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 1217 AA; 135500 MW; 1D1656F460E38508 CRC64;

Query Match 7.5%; Score 93; DB 5; Length 1217;
Best Local Similarity 23.6%; Pred. No. 1.7; Mismatches 68; Indels 22; Gaps 6;
Matches 38; Conservative 33;

QY 83 MERKTVASKMOGL---LERVTEIHFTKCAFQPPSCLEFVQNTNSRLQETSQY 139
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 627 MDVAWVADGTCKYSSVIDALEKLTMDLDFOKYKFEAPATLKAHL---FFASYASMLA 682

QY 140 ALKAPWITRONFSRCLELQCQPDSTL---PPWSPRPLEATAPAPQP-----OPLILLIL 191
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 683 ALRPQPTTSDPTAAAPVPIPNKGSILNGNPSFSPPLLPVASSIPATPESNMILYII 742

QY 192 LPVGLILLAA-----AMCLHMQRTRRRPRGEGQVPPVPSP 227
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
DB 743 GAVGGLLVAAIGVILFVFVFOKKKKEDKPD--PPAPLP 781

RESULT 13
Q9GYA1 PRELIMINARY; PRT; 560 AA.

AC Q9GYA1; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PROBABLE SURFACE ANTIGEN PROTEIN.
GN LM12.14.
OS Leishmania major.
OC Eukaryota; Euzlenzoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC01954.2; -
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR001611; IRR.
DR Pfam; PF00560; IRR; 13.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_4.
SQ SEQUENCE 560 AA; 60447 MW; C5ACF96B1059765F CRC64;

Query Match 7.4%; Score 92.5; DB 5; Length 560;

Best Local Similarity 24.8%; Pred. No. 0.75;
Matches 55; Conservative 27; Mismatches 75; Indels 65; Gaps 11;

OY 4 LAPASPTTYLLILLSSGSLGTDGCFQHSPISSDPAVKIRELSYLLQDYPVTVASN 63
DB 124 LPDWSQGLGLSVTLSCGVSGT-----LPASWGLMVRRLRELT----- 162
OY 64 LOD-EELCGGL-----W-----RLVLAQRWMEBLKTVAGSKMOGLLEVENTEIHFTVKA 112
DB 163 VADCRHLTGLSLPSLMSWLPNLOKLVRLQLOLSTLPAMSKVTSILE---LEIYAAGDIT 219
OY 113 FQPPP--SCLRFVQT-----NISRLQETSEQLVALKP-WITRON 149
DB 220 GLTPPEWSSIKSLRTLNLEGTQVSGTLPPGSEMSKSLTNLEGTQVSGSLPPQWASMAS 279
OY 150 FSRCLCQCPDSSSTLPPWSPR-----PLEATAPTPAPPP 185
DB 280 L-RTLNLGTQVSGTLPPGSEMSKSLTNLEGTQVSGTLPP 320

RESULT 14

O9HAD2 PRELIMINARY; PRT; 251 AA.

AC O9HAD2: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, last annotation update)
DE HYPOTHEICAL 26.6 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=EMBRIO;
RA Issigai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nebekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Oshima A.,
RA "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK021860; BAB13917.1;
DR InterPro; IPR002965; P-rich_extensn.
DR PRINTS; PRO1217; PRICHEXTENS.
SQ SEQUENCE 251 AA; 26607 MW; 420195B27966FD41 CRC64;

Query Match 7.4%; Score 92; DB 4; Length 251;
Best Local Similarity 31.9%; Pred. No. 0.33;
Matches 44; Conservative 9; Mismatches 39; Indels 46; Gaps 10;

OY 115 PPSCLRFVQTNIS-----RLQETSEQLVALKPWITRONFSCLELQCPDSSSTLPPW 169
DB 76 PPSCLRFVQTNIS-----ALAPQGHPEFSS--RWTFPRITTOQAPPPG 127
OY 170 SPRPL-ENTAP-----TADOPRLILLLLPVGLILLAAACLHWQTRRRPRPG 218
DB 128 PRPLPQALVPRQDPHSSPRITTOQAPPL-----W-LHPRIT--QTPPPG 169
OY 219 EQVPRVPSQDLL-LVEN 235
DB 170 ---PPRLPQALAPLADH 184

RESULT 15

O9GYAO PRELIMINARY; PRT; 536 AA.

AC O9GYAO: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 18, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROBABLE SURFACE ANTIGEN PROTEIN.

GN LM12.16.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC01955.2;
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 22.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_7.
SQ SEQUENCE 536 AA; 58020 MW; 41E16B64F667340 CRC64;

Query Match 7.3%; Score 90.5; DB 5; Length 536;
Best Local Similarity 27.2%; Pred. No. 1.1;
Matches 55; Conservative 23; Mismatches 75; Indels 49; Gaps 11;

OY 4 LAPASPTTYLLILLSSGSLGTDGCFQHSPISSDPAVKIRELSYLLQDYPVTVASN 63
DB 124 LPDWSQGLGLSVTLSCGVSGT-----LPASWGLMVRRLRELT----- 162
OY 64 LOD-EELCGGL-----W-----RLVLAQRWMEBLKTVAGSKMOGLLEVENTEIHFTVKA 112
DB 163 VADCRHLTGLSLPSLMSWLPNLOKLVRLQLOLSTLPAMSKVTSILE---LEIYAAGDIT 219
OY 113 FQPPP--SCLRFVQTNISRLQETSEQLVALKP-WITRONFSCLELQCPDSSSTLPPW 169
DB 220 GLTPPEWSSIKSLRT-----LNLEGTQVSGTLPPGSEMSKSLTN-LELGTQVSGTLPPGW 274
OY 170 S-----PPLEATAPTPAPPP 185
DB 275 SSIKSLRTLNLEGTQVSGSLPP 296

RESULT 16

O9GY15 PRELIMINARY; PRT; 660 AA.

AC O9GY15: 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PROBABLE SURFACE ANTIGEN PROTEIN.
GN LM12.151.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
RA Oliver K.,
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAC02034.2;
DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00560; LRR; 22.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_7.
SQ SEQUENCE 660 AA; 71216 MW; E213F39BF1A57BD CRC64;

Query Match 7.3%; Score 90.5; DB 5; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.5;
Matches 55; Conservative 23; Mismatches 75; Indels 49; Gaps 11;

OY 4 LAPASPTTYLLILLSSGSLGTDGCFQHSPISSDPAVKIRELSYLLQDYPVTVASN 63
DB 8 LPDWSQGLGLSVTLSCGVSGT-----LPASWGLMVRRLRELT----- 46

QY 64 LOD-EELCGGL-----W-----RLVLAORMERLKTVAAGSKMOGLERVNTEIHFVTKCA 112
Db 47 VRDCRHITGSLPSLWSLPLNIOKLVLKQLOLQSLTPAEMRSVSLF---LEIYAAGDIT 103
QY 113 FQPPP--SCLEFVOTNISRLLOETSEOLVALKP-WITRONFSRCLQCPDSSSTLPPW 169
Db 104 GTLPPEWSSIKSLRT-----LNLFGTVSGTLPPGWSMKSLTN-LELEGGVQVSGTILPPG 158
QY 170 S-----PRELEATAPPAPOP 185
Db 159 SSIKSLRTNLNEGTVSGSLPP 180

RESULT 17

Q9PU36 PRELIMINARY; PRT; 5120 AA.
AC Q9PU36;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ACZONIN (FRAGMENT).
GN ACZ.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=99439764; PubMed=10508862;
RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
RT Killmann M.W.:
"Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT zones, shares homology regions with rim and bassoon and binds
RT profilin.";
RT J. Cell Biol. 147:151-162(1999).
RL EMBL: Y19187; CAB60725.1; .
DR HSSP: P04410; 1A25.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR002965; P_rich_extensn.
DR InterPro: IPR001565; Synaptotagmin.
DR Pfam: PF00168; C2; 2.
DR Pfam: PF00595; PDZ; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR01217; PRICEXTENSN.
DR PRINTS: PR00399; SYNAPTOTAGMN.
DR SMART: SM00239; C2; 2.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; UNKNOWN_1.
DR PROSITE: PS00004; C2_DOMAIN_2; 2.
DR PROSITE: PS50106; PDZ; 1.
FT NON_TER 1
SQ SEQUENCE 5120 AA; 560751 MW; A658D9891B65B412 CRC64;

Query Match 7.3%; Score 90.5; DB 13; Length 5120;
Best Local Similarity 24.3%; Pred. No. 17;
Matches 45; Conservative 19; Mismatches 72; Indels 49; Gaps 7;

QY 90 AGSKMOGLERVNTEIHF-----VTKAFQPPSCARFVQTN----- 126
Db 2224 AARKMSYVETGIKIHEDSHKELSDMTRLNLGTATSEOPPLCVASVSEKPEASETPA 2283
QY 127 --ISRLLOETSE-QLVALPWTIRONF-----SRCLQCPDSSSTLPPWSPPLEATAP 179
Db 2284 VPRPRVSKSTYSMPSSAPALTSKVFSLFRSSSLDSPAPQSPSPPPPPPPPPPPPPPP 2343
QY 180 TAPQ-----PLILLLPVGLLLAAACILH-WQTRRRTPRPGEV 221
Db 2344 ILPKPAIYPRKKSQIOAPMATPTAVPLVTSATLESAAVLKNHVVPRVKTGTPP-PRV 2402

QY 222 PPVPS 226
Db 2403 PPVPS 2407

RESULT 18

Q17610 PRELIMINARY; PRT; 474 AA.
AC Q17610;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE C28D4.2 PROTEIN.
GN Caenorhabditis elegans.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurtry A.A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z82259; CAB05129.1; .
DR InterPro: IPR002573; Choline_kinase.
DR Pfam: PF01633; Choline_kinase; 1.
SQ SEQUENCE 474 AA; 54628 MW; DDF11C97A1542FEC CRC64;

Query Match 7.2%; Score 89.5; DB 5; Length 474;
Best Local Similarity 24.1%; Pred. No. 1.2;
Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY 27 TODC-----SFOHS-PISSDPAVKIREL-SDYLLQDYFVTVASNLQDELCGLMRL 76
Db 65 TIDCVDLKVFSPKFDSSAPISGEILFRAPFLCAKYL-----GGAMRK 106
QY 77 VLAQRMERLKTVAAGSKMOGLERVNTEIHFVTKCAFPQPPSCAR-FVQTNISRLQET- 134
Db 107 VKIEEF--RIRAITGG-MSNLIETVELPAH-LTPIQMEPEKALLRVHQSDIDILLESV 162
QY 135 -----SEOLVALKPWITTRONFSRCLQCPDSSSTLPPWSPR-PLEATA 178
Db 163 VFTLLSERNLGPKMLGVPPGGREFQIFSRALQCLEISKPELSKLIADIVARVHTLDAP 222
QY 179 PTAPOPPLILLLPVGLLLAAACILH-WQTRRRTP---RPGE-----QVPPVPSPOD 229
Db 223 PREPQ-----LTQTAQWLERF-----KKTGAGEPRIMLYLQAKVPKSDYPS 266
QY 230 LLIVE 234
Db 267 ITVAQ 271

RESULT 19

Q9UMT1 PRELIMINARY; PRT; 270 AA.
AC Q9UMT1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NK44RG2 PROTEIN.
GN NK44RG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;

[1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=LYMPHOID;
 RA Cantoni C., Blassoni R.;
 RT "Mkp4 related genes";
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ010100; CAB52290.1;
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00409; IG_1.
 SQ SEQUENCE 270 AA; 29678 MW; 327AD57A5634AE46 CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 270;
 Best Local Similarity 23.0%; Pred. No. 0.8; 112; Indels 77; Gaps 15;
 Matches 63; Conservative 22; Mismatches 63; Indels 77; Gaps 15;

QY 7 AMSPTVYLLLLLSGLSGTODCSFQHSPISSDFAVKIRELSDYLDYDPTVYASNLQD 66
 DB 2 AMRALHPLLLLLLFPGSQASKAQLVQSVAGQTLVRCQ-----YPT----- 45
 QY 67 EELGGIM-----RLVLAQR-----MMERLKYAGSKMOGLERVTET- 105
 DB 46 ---GSLYEKKGWCKEASALVCLRLVTSKPRITWMTSRF-TWDDPDAGFTVTMTDLR 100
 QY 106 ---HFVTKCAFQPPPSCLRFVQTNISRLLOETSEQLVALKFWITRONFSRCLEIQ-CQ 159
 DB 101 EEDSGH--WCRIYRPD--NSVSKSVRYFLIVSPASASQOTWTPRDVLSQOTQOSCV 156
 QY 160 PDS-----STLPPWSP-RPLDAPAPAPQ-----PILLLLLPV---GLI--- 197
 DB 157 PPTAGARQAEPSPTIIVPSHSPPLVPPLPSRQNSTLRPAPALATVPVCGLIVAK 216
 QY 198 -LLAAMCLHMQRRTRRTPRGEQV--PVPSQ 228
 DB 217 SLVSLALIVWVYLRNRMQHGRLHPAPQRPQ 250

RESULT 20
 Q9AMJ4
 ID Q9AMJ4 PRELIMINARY; PRT; 404 AA.

AC Q9AMJ4; 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, last annotation update)
 DE P0489A05.3 PROTEIN.
 GN P0489A05.3
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euhartioideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0489A05.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003105; BAB32983.1;
 DR InterPro: IPR000480; Glutein.
 DR PRINTS; PR00211; GLUTELIN.
 SQ SEQUENCE 404 AA; 43109 MW; 7CA66FDE7772A64B CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 404;
 Best Local Similarity 26.1%; Pred. No. 1.3; 88; Indels 75; Gaps 17;
 Matches 66; Conservative 24; Mismatches 66; Indels 75; Gaps 17;

QY 4.33 QHSPISSPF--AVKIRESDYLDYDPTVYASNL-----QDEELCGIMRLVL 78
 DB 107 RHSELSFSELEKVOITPLKTVWSMNPPLKPKNQFTFLTRYQMKNSPEQLCKRFW---- 162

QY 79 AQRMMERLKYAGSKMOG---LLERVNT--ELHFVKCAFQPPPSCLRFVQTNI---SRL 130
 DB 163 -STWOSNAGAV-GSRAGSERILRRPSSAGRRPMLVPPSPPPASLAAQPNALTSRA 220
 QY 131 LOETSEQLVALKFWITRONFSR---CLEIQ-CQPDSTLP-----PPWSRPLEAT 177
 DB 221 LSATG-----TPTTSSILRRPLHCLLPRLAPRPPSILPLPLQAPPHPPLP---P 271
 QY 178 APTAQPPPLLLLL-----PV---GLL-----LLAAMCLHMQRTRRRTPR 216
 DB 272 PPTARAPPLAVCLRLCPILPKPPVAGGLFVAHSAITVLAQAGCV--RLHRRPLR 329
 QY 217 P--GEQVPPVPS 227
 DB 330 PPSSELLPLSRAP 342

RESULT 21
 Q943D5
 ID Q943D5 PRELIMINARY; PRT; 1267 AA.
 AC Q943D5; 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE PUTATIVE RECEPTOR SERINE/THREONINE KINASE.
 GN P0443D08.17.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Euhartioideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0443D08.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003250; BAB64138.1;
 KW Receptor; Kinase.
 SQ SEQUENCE 1267 AA; 136583 MW; 062P0C27C5490D75 CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 1267;
 Best Local Similarity 22.0%; Pred. No. 5; 96; Indels 71; Gaps 11;
 Matches 54; Conservative 24; Mismatches 96; Indels 71; Gaps 11;

QY 22 SGLSGTQDCSPQHS---PISSDFAVKIRELSDYLDYDPTVYASNLQDEELCGIMRLV 77
 DB 725 AREGTAPCDLRRGIVVVVADPAARARKTEAGTQ---TEGGRWSSPACGGRAAAS 780
 QY 78 LAQRMMERLKYAGSKMOGLERVTETIHFVKCAFQPPPSCLRFVQTNISRLLOETSEQ 137
 DB 781 RARR-----KEBAGARGVYTAARRSSP-----ARKGEARPPDLRLI-----YPAANGS 824
 QY 138 LVALKFWITRONFSRCLEIQCPDSSSTLPWPSPRPLEATAPTA----- 181
 DB 825 TACTPWPPELHHN-----RCSSSSSSSPSP--PRLGATAPTAARCSHKSAPPRAVPSD 876
 QY 182 -----PQPLLLLLLP-----VGLLLLAAMCLH--WQRRRTTRPRGEGVPPVP 225
 DB 877 RRRRLSSPPPPQIVAAAPSDRRRLGPPQIAAAALHHNEWALA-----GQCLTFPP 929
 QY 226 SPQDL 230
 DB 930 PPPQL 934

RESULT 22
 ID 075064 PRELIMINARY; PRT; 1386 AA.
 AC 075064;

DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIA0476 PROTEIN.
 GN KIA0476.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=98116662; PubMed=9455484;
 RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
 Nomura N., Ohara O.;
 RT "Characterization of cDNA clones in size-fractionated cDNA libraries
 from human brain";
 RL DNA Res. 4:345-349(1997).
 DR EMBL; AB007945; BAA32321.1; .
 DR InterPro; IPR001194; DENN.
 DR InterPro; IPR002885; PPR.
 DR Pfam; PF02141; DENN; 1.
 DR Pfam; PF01535; PPR; 1.
 DR SEQUENCE 1386 AA; 152297 MW; BE960E7169A7EFDA CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 1386;
 Best Local Similarity 23.1%; Pred. No. 5.6;
 Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;
 QY 21 SSGLSSTOCPSFOHSPISDFVAKRELSDVILQDYPYVANSNODELCL---GGLMRL 76
 DB 1104 SAGASSSKDAPYVGGP- - - - -GPVLSRRRLCLTA--LDEPOLCGHMGASRR 1148
 QY 77 VLAORMERLKTVAASKMOGLERVTNTEHFVTKCAFQPPSCRFVOTNISRLLQETSE 136
 DB 1149 VESGAWAYLSPVLRLRELESLVENEGSEV- - - - -LALPELSAHLIPWNLWYFQRL- 1201
 QY 137 QVAAKPMTRTNRNFSRCLELQCO-PDSSLTLPWP-SPRPLA- - - - -TATAPQPP 185
 DB 1202 RLPSILIPGVNLAS- - - - -CDGFSHSDQVSPWLTTPPASVQVRLMDVLTLPSPNSCP 1253
 QY 186 LLLLLLPVGLLLAAWCLMORTRRTPRPPGCVPPVPSPODLLAVE 234
 DB 1254 LVYL- - - - -WRVHSQ-IPQRVWVG- - - - -VPVASTSLALLE 1284

RESULT 23
 ID Q9GKE2 PRELIMINARY; PRT; 250 AA.
 AC Q9GKE2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE SR-PSOX.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_Taxid=9823;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20576214; PubMed=11060282;
 RA Shinooka T., Kume N., Minami M., Hayashida K., Kataoka H., Kita T.,
 Yonehara S.;
 RT "Molecular Cloning of a Novel Scavenger Receptor for Oxidized Low
 Density Lipoprotein, SR-PSOX, on Macrophages";
 RL J. Biol. Chem. 275:40663-40666(2000).
 DR EMBL; AF277000; AAG31753.1; .
 DR SEQUENCE 250 AA; 27569 MW; 6A4DCFA55C35421E CRC64;

Query Match 7.1%; Score 88; DB 6; Length 250;
 Best Local Similarity 24.2%; Pred. No. 0.82;

Matches 64; Conservative 33; Mismatches 100; Indels 68; Gaps 14;

QY 6 PMAWPTYLILLILL- - - - -SSGLSGTQDCS---FQHSPISSDFANKIELSDYL- 52
 DB 2 PUMELMFFLLALFLAMLPPNGNMGSMAGSCPNNRRISSHSPTDH--DMRLKRLTYLN 58
 QY 53 -LQDYPVIVASLQDEELCGGLMRLVLAORWNERL- - - - -KTVAASKMOGL 97
 DB 59 HYQCHSTYVRQLPRGSCGG- - - - -SSDQVYKLKMGCFDRGEGRAHARTVA---HQCH 110
 QY 98 LERVNTEHFVTKCAFQPPSCFLRFVOTNISRLLQETSEDLVAIKPWITR--QNSRCLE 155
 DB 111 LAPONTTRVPELPERA- - - - -PPDSTPAQTNPSTQPTQ- - - - -KPLPEGMPSLAKKIL 161
 QY 156 LQCPDSSSTLPWPSPRP- - - - -LEATAPAPQPP- - - - -LILLLLPVGILLTA 200
 DB 162 PISENDISTVGSLSLCAKSEARENDEQLCKNGATGTSALVPVLSLVYIFLLTGVLTY- 220
 QY 201 AAWCLMORTRRTPRPPGCVPPV 225
 DB 221 -VMCKKRQEQSHQYP-PDPQLHYVP 243

RESULT 24
 ID Q9DBT2 PRELIMINARY; PRT; 675 AA.
 AC Q9DBT2;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 1200014H2ARIK PROTEIN.
 GN 1200014H2ARIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_Taxid=10090;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=LUNG;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiba H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner U., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Welte C., Whitaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK004763; BAB23544.1; .
 DR HSSP; Q15843; 1INDD
 DR MGD; MGI:1914715; 1200014H2ARIK.
 DR InterPro; IPR002965; P_rich_extensn.
 DR InterPro; IPR000061; Surp.
 DR InterPro; IPR000626; Dbligultin.
 DR Pfam; PF01805; Surp; 1.
 DR Pfam; PF00240; ubiigultin; 1.
 DR PRINTS; PR01217; PRICHEXTENSN.
 DR SMART; SM00213; UBO; 1.
 DR PROSITE; PS50053; UBIQUITIN_2; 1
 DR SEQUENCE 675 AA; 75703 MW; 3039679A63ED85EF CRC64;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:34:09 ; Search time 53.63 Seconds

(without alignments)
486.712 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MTVLAPAPMSPTYLILLLL.....RPGSQVPPVSPQDLLVEH 235

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A.Geneseq_032802:*
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20: /SID55/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SID55/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SID55/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	16 AAR67541	Human flt-3 ligand
2	1242	100.0	235	20 AAR67769	Human flt3-ligand
3	1242	100.0	235	21 AAY69719	Full length wild t
4	1242	100.0	235	22 AAB20192	Human flt-3 ligand
5	1236	99.5	235	16 AAR66175	Human S86/S109 flt
6	1236	99.5	235	22 AAB20194	Human flt-3 ligand
7	1124	89.7	209	19 AAY69721	Human flt-3 mutain
8	1114	89.7	209	19 AAY69707	Human flt-3 recept
9	1114	89.7	209	21 AAY69720	Mature wild type h
10	1110	89.4	209	21 AAY69723	Human flt-3 mutain
11	1110	89.4	209	21 AAY69726	Human flt-3 mutain

12	1110	89.4	209	21 AAY69727	Human flt-3 mutain
13	1108	89.2	209	21 AAY69729	Human flt-3 mutain
14	1108	89.2	209	21 AAY69722	Human flt-3 mutain
15	1107	89.1	209	21 AAY69724	Human flt-3 mutain
16	1107	89.1	209	21 AAY69728	Human flt-3 mutain
17	1100	88.6	209	21 AAY69725	Human flt-3 mutain
18	970	78.1	185	22 AAB20195	Human flt-3 ligand
19	895.5	72.1	294	21 AAY58204	Canine flt-3 ligand
20	894.5	72.0	291	21 AAY58210	Feline flt-3 ligand
21	834	67.1	178	22 AAB20193	Human flt-3 ligand
22	797.5	64.2	268	21 AAY58206	Canine mature flt-
23	796.5	64.1	276	21 AAY58207	Canine flt-3 ligand
24	791.5	63.7	265	21 AAY58211	Feline mature flt-
25	768.5	61.9	231	16 AAR67540	Mouse flt-3 ligand
26	768.5	61.9	231	20 AAR67768	Murine flt3-ligand
27	768.5	61.9	231	22 AAB20186	Mouse flt-3 ligand
28	768	61.8	232	16 AAR66177	Mouse M0T110/T118
29	764	61.5	232	22 AAB20189	Mouse flt-3 ligand
30	745	60.0	150	19 AAW77930	Flt3 ligand FLT10C
31	745	60.0	150	19 AAM69054	Human flt-3 recept
32	740.5	59.6	377	19 AAW78124	Chimeric receptor
33	739	59.5	143	19 AAW77926	Flt3 ligand FLT3C.
34	739	59.5	143	19 AAM69050	Human flt-3 recept
35	737.5	59.4	349	19 AAM63289	Human flt3 ligand
36	737.5	59.4	349	19 AAW78005	Human flt3 ligand
37	736.5	59.3	340	19 AAW83291	Flt3L 1-139/IG2b/
38	736.5	59.3	349	19 AAM63286	Human flt3 ligand
39	736.5	59.3	523	19 AAW78008	Human flt3 ligand
40	735	59.2	140	19 AAW77911	Trimeric Flt3L-G-C
41	735	59.2	140	19 AAM69035	Human flt3 ligand
42	735	59.2	144	19 AAW77928	Flt3 ligand FLT4C.
43	735	59.2	144	19 AAM69052	Human flt-3 recept
44	735	59.2	313	19 AAM63294	Human flt3 ligand
45	733.5	59.1	286	19 AAM63303	Human flt3 ligand
46	733.5	59.1	286	19 AAW77952	Flt-3 and IL-3 chl
47	733.5	59.1	314	19 AAM63293	Human flt3 ligand
48	733.5	59.1	314	19 AAW78004	Dimeric Flt3 ligand
49	733.5	59.1	460	19 AAW78007	Trimeric flt-3 rece
50	733.5	59.1	523	19 AAW78006	Trimeric Flt3L-G-C

ALIGNMENTS

RESULT 1	
ID	AAR67541 standard; Protein; 235 AA.
XX	
AC	AAR67541;
XX	
DT	05-AUG-1995 (first entry)
XX	
DE	Human flt-3 ligand.
XX	
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX	
OS	Homo sapiens.
XX	
FH	Location/Qualifiers
FT	1..26
FT	/label= Sig peptide
FT	/note= "signal peptide may extend to position 27"
FT	27..182
FT	/label= Extracellular domain
FT	/note= "extracellular domain may start at position 28"
FT	183..205
FT	/label= Transmembrane domain
FT	206..235
FT	/label= Cytoplasmic domain
XX	
PN	EPE27487-A.
XX	

PE 12-JUN-1998; 98WC-US12085.
XX
PR 17-JUN-1997; 97US-0877421.
XX
PA (IMM) IMMUNE CORP.
XX
PI Abbott NM, Mowat AM, Viney JL;
XX WPI; 1999-070422/06.
DR N-PADB; AAW81506.
XX
PT Methods for initiating or enhancing antigen specific immune
PT tolerance - By using murine or human flt3 ligand
XX
PS Claim 1; Page 14-15; 25pp; English.

A method has been developed of initiating or enhancing: (i) an antigen-specific immune tolerance; or (ii) immunotolerance of a therapeutic CC
CC immunogenic molecule by addition of a polypeptide, before, after or with CC
CC the mucosal administration of an immunotolerising amount of the antigen CC
or therapeutic molecule, respectively. The polypeptide is capable of CC
binding the flt3 receptor and is: a) amino acids 28-x of murine flt3 CC
ligand (flt3-L), where x is an amino acid between 163-231; b) amino CC
acids 28-y of human flt3-L, where y is an amino acid between 160-235; CC
and c) a polypeptide that has at least 90% identity to the polypeptides CC
of either (a) or (b). The method ameliorates the effects of autoimmune CC
diseases, food allergies or organ or tissue rejection following CC
transplantation. Administration of flt3-L allows lower doses of antigens CC
to be used in vivo for mucosally administered antigens. The present CC
sequence represents human flt3-L.

Query Match	100.0%	Score 1242;	DB 20;	Length 235;
Best Local Similarity	100.0%	Pred. No. 4.1e-109;		
Matches 235;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY 1	MTVLAPAMSPPTYLIIILLISGLSGTQDCQFQHPISDSDFAVKIRREISDYLLQDYPYTV 60			
Db 1	mtvlapamspptylIIIIIIIIISGLSGTQDCSGHNPISDSDFAVKIRREISDYLLQDYPYTV 60			
QY 61	ASNLQDEELCGGLMRLVLAQRMWERIKTVAGSKMOGLLERVNTEIHEVTKCAFQPPSC 120			
Db 61	asnlqdeelcggllwrlvlagrmwerlktvagskmgllervnteihfvtkcafqppsc 120			
QY 121	RFQVQTNSTRLLQTSFQVLAIKPMITRQFNSCLELQCPQSSSTLPFPMSPRPLEAAPT 180			
Db 121	rfgvtnstrlllqetseqvalkpwlltrqftrcfelelqcqpdssstlpppwsprpleaatp 180			
QY 181	APQPPDLLLILLYGGLLLAAAMCLMHQTRRRTRPRGBOYPPVPSDDLIVHE 235			
Db 181	apqppllllllllpyglIIIIlaaawclhwqtrrrrrtrppsgqyppvpsqdlllveh 235			

RESULT	3
AAV69719	
ID	AAV69719 standard; Protein; 235 AA.
XX	
AC	AAV69719;
XX	
DT	05-JUL-2000 (first entry)
XX	
DE	Full length wild type human flt-3 protein.
XX	
KW	Immunomodulator; immunosuppressive; cytostatic; anti-HIV;
KW	neuroprotective; antitalleritic; flt3 ligand; flt3-L; wild type; allergy;
KW	cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW	cellular expansion; cellular differentiation; natural killer cell;
KW	cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW	myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW	multiple myeloma; leukemia.
XX	

OS Homo sapiens.
 XX
 PN W0200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 25-JUN-1999; 99MO-US14296.
 XX
 PR 02-JUL-1998; 98US-0109100.
 XX
 PA (IMMV) IMMUNEX CORP.
 PI Graddis TJ, McGrew JT;
 XX WPI: 2000-182115/16.
 DR N-PSDB; AAZ59064.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions,
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 PS
 PS Claim 1; Page 72-73; 90pp; English.
 XX
 XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (this sequence) or mature (AA69720) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 CC
 CC Sequence 235 AA;
 SQ
 Query Match 100.0%; Score 1242; DB 21; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAMSPPTYYLLLLSSGSGTDCSFQHSPISSDPAVKIRELSDYLDYDPYTV 60
 DB 1 mtvlapamsppttylllllssgsgtcdcfqhspsissdtafvkirelsdyllqdyptv 60
 QY 61 ASNIDEEELCGGLMRLVLAORMERLKTVAAGSKMGGILLERVNTEIHFTKCAFQPPPSCL 120
 DB 61 asnldeeelcggllmrlvlaormerlktvagskmgillervnteihftkcafqpppscl 120
 QY 121 RRVQVNIIRLQDETSEQLVKLPWITTRNFSCRLQLCOQPPSSITLPPWSSRPLEATAPT 180
 DB 121 rrvqvnirrlqdetseqlvklpwittrnfsrclqlcoqppsstlppwssrpleatapt 180
 QY 181 AFQPELLELLLPVGLLLAAAMCLHMQRTRRRPRPGEQVPPVPSDDLLVEH 235
 DB 181 aqppllllllllpvgllllaaawclhmqrtrrrprpgeqvpvpspdlllveh 235

XX
 XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..26
 FT /Label= Signal_peptide
 FT 27..235
 FT Protein /Label= Mature_protein
 FT 27..182
 FT Domain /Label= Extracellular_domain
 FT 183..205
 FT Domain /Label= Transmembrane_domain
 FT 206..235
 FT Domain /Label= Cytoplasmic_domain
 XX
 PN W0200109303-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 31-JUL-2000; 2000MO-US20679.
 XX
 PR 30-JUL-1999; 99US-0146170.
 XX
 PA (VICA-) VICAL INC.
 XX
 PI Hermanson GG;
 XX
 DR WPI: 2001-123319/13.
 DR N-PSDB; AAF30310.
 XX
 PS Immunogenic compositions comprising Flt-3 ligand encoding
 PS polynucleotide and one or more antigen, or cytokine encoding
 PT polynucleotides, useful for suppressing tumour growth and for treating
 PT autoimmune diseases (e.g. rheumatoid arthritis) -
 XX
 XX Claim 2; Page 132-133; 149pp; English.
 PS
 PS The present sequence is that of human Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen or
 CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
 CC polynucleotide may encode the present full-length human Flt-3
 CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
 CC or 27-235 of the ligand. The polynucleotides are incorporated
 CC into the cells of the vertebrate in vivo, and a prophylactically
 CC or therapeutically effective amount of Flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.
 CC
 CC Sequence 235 AA;
 XX
 SQ
 Query Match 100.0%; Score 1242; DB 22; Length 235;
 Best Local Similarity 100.0%; Pred. No. 4.1e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAMSPPTYYLLLLSSGSGTDCSFQHSPISSDPAVKIRELSDYLDYDPYTV 60
 |||

CC The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present full-length human Flt-3
CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235
CC of the Flt-3 ligand. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.

CC
XX
SQ Sequence 235 AA:

Query Match 99.5%; Score 1236; DB 22; Length 235;
Best Local Similarity 99.6%; Pred. No. 1.5e-108;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYTLPARMSFTYLLLLLSGLSTGDCSFQHSPISSDFANKIELSDYLLQDYPVYV 60
DB 1 MYLAPAWSPTLYLIIIIISGISGTCDSIQHSPISSDFAVKIRELSdyllqdyprv 60
QY 61 ASNLODELCGGLMRLVLAQRMRERLKTVAAGSKMGLLERVTEHFVTKAFQPPSC 120
DB 61 asnlqdeclcgglwrlvlagrmrerkltvagskmqgllevrnteifvckatqppsc 120
QY 121 RFVQTNISRLQETSEQLVAKFWITRONFSRCLFELQCPDSTLPPMSPRLEATAT 180
DB 121 rfvgtnisrlqetseqlvakfwitrgnfsrclfqcpdstlppwsprileaapt 180
QY 181 APOPLLLLLLPVGLLLAAAMCLMORTRRTPRPGEOVPVPSPODLLVEH 235
DB 181 apopllylllllpvgllllaaawclmwgrtrrrtprpgeqvppspqdlllveh 235

RESULT 7

AA69721
ID AAY69721 standard; protein; 212 AA.

XX
AC AAY69721;

DT 05-JUL-2000 (first entry)

XX
DE Human flt-3 mutein L-3H.

KW Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;
KW neuroprotective; anti-allergic; Flt3 ligand; Flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.

XX
OS Homo sapiens.
OS Synthetic.

PN WO200001823-A2.

XX
PD 13-JAN-2000.

XX
PF 25-JUN-1999; 99WO-US14296.

XX
PR 02-JUL-1998; 98US-0109100.

XX
PA (IMMUNEX CORP.

XX
PI Graddis TJ, McGrew JT;

XX
DR WPI; 2000-182115/16.

PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX
XX Claim 4; Page 79-80; 90pp; English.

PS The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
XX which exhibits increased or decreased biological activity relative to
XX the full length wild type (AAY69719) or mature (AAY69720) flt3-L
XX polypeptides. This sequence represents an example of the novel flt-3
XX ligands and comprises the L-3H mutant polypeptide. The flt3-L protein
XX binds cell surface tyrosine kinase receptors and regulate growth and
XX differentiation of hematopoietic progenitor cells. The flt3-L protein can
XX be used to induce cellular expansion (especially in vivo) or
XX differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
XX cells, especially in the presence of growth factors such as interleukins,
XX colony stimulating factors or protein kinases. The protein can also
XX modulate, augment or enhance a patient's immune response and can be used
XX to treat an immune disorder (e.g. allergy, autoimmunity or
XX immunosuppression). The protein may be used to treat a pathological
XX condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
XX small cell lung, testicular, aplastic anemia, HIV infection, breast,
XX myeloma, neuroblastoma or acute leukemia.

XX
SQ Sequence 212 AA:

Query Match 90.5%; Score 1124; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.9e-98;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SCTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTASNLODELCGLMRLVLAQRME 84
DB 2 sctqdcsfqhspsiddfavkirelsdyllqdyprvtaasnlqdeclcgglwrlvlagrme 61
QY 85 RKTIVAGSKMGLERVNTTEHFVTKAFQPPSCRLRVQTNISRLQETSEQLVAKPW 144
DB 62 rktivagskmqgllevrnteifvckatqppscrlrvqtnisrlqetseqlvakpw 121
QY 145 ITRONFSRCLFELQCPDSTLPPMSPRLEATATAPOPPLLLLPVGLLLAAAMC 204
DB 122 itrqnfsrclfqcpdstlppwsprileaaptappplllllllpvglllilaawc 181
QY 205 LHMORTRRTPRPGEOVPVPSPODLLVEH 235
DB 182 lhwgrtrrrtprpgeqvppspqdlllveh 212

RESULT 8

AA69007
ID AAY69007 standard; peptide; 209 AA.

XX
AC AAY69007;

DT 01-OCT-1998 (first entry)

XX
DE Human flt-3 receptor agonist.

KW Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
KW bone marrow reconstitution; haematological disease; immune deficiency;
KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
KW congenital metabolic disease; neurological disease; therapy;
KW dendritic cell production.

OS Homo sapiens.
 XX
 XX WO9818923-A1.
 XX
 PD 07-MAY-1998.
 XX
 XX 23-OCT-1997; 97WO-US18700.
 XX
 XX 25-OCT-1996; 96US-0030094.
 XX
 XX (SEAR) SEARLE & CO G D.
 PA
 PI Feng Y, McKearn JP, McWhirter CA, Minnerly JC, Munster NI;
 PI Staten NR, Streeter PR, Wolfe SL;
 XX
 DR WPI: 1998-272218/24.
 XX
 PT Rearranged flt-3 receptor agonists and nucleic acids encoding them -
 PT used to stimulate production of haematopoietic and dendritic cells,
 PT for treatment of haematological diseases, bone marrow reconstitution
 PT and in gene therapy
 PS
 PS Disclosure: Page 9-10; 158bp; English.
 XX
 CC This sequence represents a rearranged human flt-3 receptor agonists of
 CC the invention. The agonists have a modified flt-3 ligand amino acid
 CC sequence. The agonists are used to stimulate production of haematopoietic
 CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
 CC expansion for subsequent transplantation, e.g. to reconstitute bone
 CC marrow after chemotherapy, disease etc., or to treat haematological
 CC disease such as drug-induced myelosuppression, defects caused by
 CC infections, burns or renal dialysis. Optionally ex vivo expanded cells
 CC are transduced with a gene therapy vector for treating e.g. congenital
 CC metabolic diseases, immune deficiency, neurological disease, cancer and
 CC infections. The agonists can also be used in the treatment of tumours,
 CC infections and autoimmune disease, when administered optionally with an
 CC antigen. The agonist can also be used in the production of dendritic
 CC cells for use as an immunising adjuvant for treatment disorders including
 CC acquired immune deficiency syndrome. Compared with native ligands, the
 CC new agonists have better stimulatory activity, reduced side effects
 CC and/or better physical properties such as solubility, stability or re-fold
 CC efficiency. When used together with other stimulatory agents, the
 CC agonists provide a synergistic effect.
 CC
 XX
 XX Sequence 209 AA;
 SQ
 Query Match 89.7%; Score 1114; DB 19; Length 209;
 Best Local Similarity 100.0%; Pred. No. 4.2e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TODCSFOHSPISDPAVKIRELSDYLLQDYPTVASNLQDELCGMLRLVLAQRMERL 86
 DB 1 tqdcsfqhpissdfavkirelsdyllqdyptvasnlgdeelcgglwrlvlaqrmmerl 60
 QY 87 KTVAGSKMOGLLEVRNTEHFYTKARQPPSCLEFVQTNISRLQETSEDLVAKFWIT 146
 DB 61 ktvagskmqgllervnteihfvtkcaroppsscrlrfvqtnisrlqetseqlvalkpwit 120
 QY 147 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLILPVGILLAAACILH 206
 DB 121 rqnsrclelqcpdssstlppwsprrpleatcapapqppllllllpvgllllaaacilh 180
 QY 207 WQTRRRTRPRGQVPPVPSODLLVEH 235
 DB 181 wqtrrrtrprgqvppvpsoDLLVEH 209
 RESULT 9
 AAY69720
 ID AAY69720 standard; Protein; 209 AA.
 XX
 AC AAY69720;

XX
 DT 05-JUL-2000 (first entry)
 XX
 XX Mature wild type human flt-3 protein.
 DE
 XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiatherogenic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200001823-A2.
 XX
 PD 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 PF
 PR 02-JUL-1998; 98US-0109100.
 XX
 XX (IMM) IMMUNEX CORP.
 PA
 XX Graddis TJ, McGrew JT;
 PI
 PI WPI: 2000-182115/16.
 DR N-PSDB; AA659064.
 XX
 XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 PS
 PS Claim 1: Page 89-90; 90pp; English.
 XX
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibit increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (this sequence) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 CC
 XX
 XX Sequence 209 AA;
 SQ
 Query Match 89.7%; Score 1114; DB 21; Length 209;
 Best Local Similarity 100.0%; Pred. No. 4.2e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TODCSFOHSPISDPAVKIRELSDYLLQDYPTVASNLQDELCGMLRLVLAQRMERL 86
 DB 1 tqdcsfqhpissdfavkirelsdyllqdyptvasnlgdeelcgglwrlvlaqrmmerl 60
 QY 87 KTVAGSKMOGLLEVRNTEHFYTKARQPPSCLEFVQTNISRLQETSEDLVAKFWIT 146
 DB 61 ktvagskmqgllervnteihfvtkcaroppsscrlrfvqtnisrlqetseqlvalkpwit 120
 QY 147 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLILPVGILLAAACILH 206
 DB 121 rqnsrclelqcpdssstlppwsprrpleatcapapqppllllllpvgllllaaacilh 180
 QY 207 WQTRRRTRPRGQVPPVPSODLLVEH 235

Db 181 wqrrrtprpgsqvpyppspqdlllleeh 209
|||||
RESULT 10
AA69723
ID AA69723 standard; Protein; 209 AA.
XX
AC AAY69723;
XX
DT 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein K84E.
XX
KW Immunomodulator; immunosuppressive; cytostatic; antineoplastic; anti-HIV;
KW neuroprotective; antitumor; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200001823-A2.
PD 13-JAN-2000.
PF 25-JUN-1999; 99WO-US14296.
PR 02-JUL-1998; 98US-0109100.
PA (IMMUNE) IMMUNEX CORP.
PI Gradtis TJ, McGrew JT;
PI WPI: 2000-182115/16.
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
PS Claim 4; Page 84-85; 90pp; English.
XX
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA:

Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1e-96; Mismatches 0; Gaps 0;
Matches 208; Conservative 1; Indels 0;

27 TQDCSFHSPFISSDFVVKTRFISDYLLDDYPYTVASNLQDELGGILMRVLQAQRWERTL 86
1 tgcgcfshpsissdfcvktrfistdyllddypvtvasnlqdeggilmrvlqaqrwermertl 60

Qy	87	KNAASKNGGLERNTNTHVTCAGQPPPSCLRFQNTISRLQETSQGLVAKPWIT	146
Db	61	KVAAASKNGGLERNTNTHVTCAGQPPPSCLRFQNTISRLQETSQGLVAKPWIT	120
Qy	147	RONFRSCHELCOOPSSSTLPMPSPRLFETAPAPQPLLLLLLPVGLLLAAAWCH	206
Db	121	rgfarsclclcgqpsstlpppsprpleatpapppllllllllpvlllllaawch	180
Qy	207	WQTRRRPRFGEQVPPPSFDLLVEH	235
Db	181	wqtrrrprfgeqvpvpspdlllvch	209
RESULT 11			
AA69726	ID	AA69726 standard; Protein; 209 AA.	
XX	AA69726;		
AC	XX		
DT	XX		
XX	05-JUL-2000 (first entry)		
DE	XX		
XX	Human flt-3 mutcin Q122R.		
KM	Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;		
KM	neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;		
KM	cell surface tyrosine kinase receptor; hematopoietic progenitor cell;		
KM	cellular expansion; cellular differentiation; natural killer cell;		
KM	cancer; dendritic cell; immune response; autoimmunity; immunosuppression;		
KM	myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;		
XX	multiple myeloma; leukemia; mutcin.		
OS	Homo sapiens.		
OS	Synthetic.		
XX	WO200001823-A2.		
PN	13-JAN-2000.		
XX			
PD	25-JUN-1999; 99WO-US14296.		
PE			
XX			
PR	02-JUL-1998; 98US-0109100.		
XX			
PA	(IMMUNEX) IMMUNEX CORP.		
XX			
PI	Graddis TJ; McGrew JT;		
XX			
DR	WPI: 2000-182115/16.		
XX			
PT	Mutant soluble flt3 ligand polypeptide used in cellular expansion,		
PT	immune response stimulation or treatment of pathological conditions		
PT	contains amino acid substitutions at positions 8, 84, 118 or 122		
XX			
XX	Claim 4; Page 88-89; 90pp; English.		
XX			
CC	The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides		
CC	which exhibits increased or decreased biological activity relative to		
CC	the full length wild type (AA69719) or mature (AA69720) flt3-L		
CC	polypeptides. This sequence represents an example of the novel flt-3		
CC	ligands and comprises the Q122R mutant polypeptide. The novel flt-3		
CC	binds cell surface tyrosine kinase receptors and regulate growth and		
CC	differentiation of hematopoietic progenitor cells. The flt3-L protein can		
CC	be used to induce cellular expansion (especially in vivo) or		
CC	differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic		
CC	cells, especially in the presence of growth factors such as interleukins,		
CC	colony stimulating factors or protein kinases. The protein can also		
CC	modulate, augment or enhance a patient's immune response and can be used		
CC	to treat an immune disorder (e.g. allergy, autoimmunity or		
CC	immunosuppression). The protein may be used to treat a pathological		
CC	condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,		
CC	small cell lung, testicular or ovarian cancer, lymphoma, multiple		
CC	myeloma, neuroblastoma or acute leukemia.		

SQ Sequence 209 AA:
 Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1e-96;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TDDCSFQHSPISSDFAVKIRELSDYLQDYPVTVASNIODEFLGGIMRWLAORWRL 86
 DB 1 tqdcstfghspissdfavkirelsdyllqdyptvasnlgdeecgllwrlvlaqrwmerl 60
 OY 87 KTVAGSKMOGLERVNTIEHFTKCAFOPPSCLEFVOTNISRLIQTSEQLVALKPWIT 146
 DB 61 ktvagskmgglervnteihfvtkcafpppsclrfvqtnisrllqetseqvalkpwilt 120
 QY 147 RQNFSCLELQCCPDSSITPPWSPRPLEATAPAPQPLLILLPVGILLAAACGLH 206
 DB 121 rnfscrlqlqcdpsstlppwsprrpleataptapqppllllllpvgllllaaacglh 180
 QY 207 WQTRRRTRPRGEGVPPVPSPODLLVLEH 235
 DB 181 wqtrrrtrprgeqvppvpspdqdlllveh 209

RESULT 12

AA69727
 ID AAY69727 standard; Protein; 209 AA.
 AC AAY69727;
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 mutetin L26F.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutetin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 PD 13-JAN-2000.
 PF 25-JUN-1999; 99WO-US14296.
 PR 02-JUL-1998; 98US-0109100.
 PA (IMMUNEX) IMMUNEX CORP.
 PI Graddis TJ, McGrew JT;
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX
 PS Claim 13; Page 82-83; 90pp; English.
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69729) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or

CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.

SQ Sequence 209 AA:

Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TDDCSFQHSPISSDFAVKIRELSDYLQDYPVTVASNIODEFLGGIMRWLAORWRL 86
 DB 1 tqdcstfghspissdfavkirelsdyllqdyptvasnlgdeecgllwrlvlaqrwmerl 60
 QY 87 KTVAGSKMOGLERVNTIEHFTKCAFOPPSCLEFVOTNISRLIQTSEQLVALKPWIT 146
 DB 61 ktvagskmgglervnteihfvtkcafpppsclrfvqtnisrllqetseqvalkpwilt 120
 QY 147 RQNFSCLELQCCPDSSITPPWSPRPLEATAPAPQPLLILLPVGILLAAACGLH 206
 DB 121 rnfscrlqlqcdpsstlppwsprrpleataptapqppllllllpvgllllaaacglh 180
 QY 207 WQTRRRTRPRGEGVPPVPSPODLLVLEH 235
 DB 181 wqtrrrtrprgeqvppvpspdqdlllveh 209

RESULT 13

AA69729
 ID AAY69729 standard; Protein; 209 AA.
 AC AAY69729;
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 mutetin A64T.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutetin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 PD 13-JAN-2000.
 PF 25-JUN-1999; 99WO-US14296.
 PR 02-JUL-1998; 98US-0109100.
 PA (IMMUNEX) IMMUNEX CORP.
 PI Graddis TJ, McGrew JT;
 DR WPI; 2000-182115/16.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX

PS Claim 13; Page 78-79; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA:

Query Match 89.4%; Score 1110; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1e-96; 1; Indels 0; Gaps 0;
Matches 208; Conservative 0; Mismatches 1;

QY 27 TDGCSFQHSPISSDPAVKIRELSDYLLQDYPVYASNLQDEELCGIMRLVLAQRMERL 86
1 tqdcsfqhspissdfavkirelsdyllqdyprvvasnqdeelcgilwrlvlaqrmerl 60
DB
QY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFQPPPSCLRFVQNTISRLQETSEQVLAKEPMT 146
1 ktvagskmgllervnteihftkcafpppsclrfvqntisrlqetseqlvalkpmit 120
DB
QY 147 RQNFSCLELQCPDSSITLPPWSPRPLEATAPAPQPLLILLPVGLLLAAWCLH 206
121 rqnfsclclqcpdssitlppwsprrpleatcapqppllllllpvgllllaaawclh 180
DB
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
1 wqtrrrtprgeqvppvpdpqdilllvh 209
DB
181 wqtrrrtprgeqvppvpdpqdilllvh 209

RESULT 14
AAV69722
ID AAV69722 standard; Protein; 209 AA.
XX
AC AAV69722;
XX
XX 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein H8Y.
XX
XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US14296.
XX
XX 02-JUL-1998; 98US-0109100.
XX

PA (IMM) IMMUNEX CORP.
XX
XX Graddis JT, McGrew JT;
XX
XX WPI; 2000-182115/16.
DR
XX
XX
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122
XX
PS Claim 4; Page 81-82; 90pp; English.
XX
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the H8Y mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
SQ Sequence 209 AA:

Query Match 89.2%; Score 1108; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.6e-96;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDGCSFQHSPISSDPAVKIRELSDYLLQDYPVYASNLQDEELCGIMRLVLAQRMERL 86
1 tqdcsfqhspissdfavkirelsdyllqdyprvvasnqdeelcgilwrlvlaqrmerl 60
DB
QY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFQPPPSCLRFVQNTISRLQETSEQVLAKEPMT 146
1 ktvagskmgllervnteihftkcafpppsclrfvqntisrlqetseqlvalkpmit 120
DB
QY 147 RQNFSCLELQCPDSSITLPPWSPRPLEATAPAPQPLLILLPVGLLLAAWCLH 206
121 rqnfsclclqcpdssitlppwsprrpleatcapqppllllllpvgllllaaawclh 180
DB
QY 207 WQTRRRTPRGEQVPPVPSQDILLVEH 235
1 wqtrrrtprgeqvppvpdpqdilllvh 209
DB
181 wqtrrrtprgeqvppvpdpqdilllvh 209

RESULT 15
AAV69724
ID AAV69724 standard; Protein; 209 AA.
XX
AC AAV69724;
XX
XX 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein K84T.
XX
XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
XX Homo sapiens.
OS

OS Synthetic.
XX PN WO200001823-A2.
XX PD 13-JAN-2000.
XX PF 25-JUN-1999; 99WO-US14296.
XX PR 02-JUL-1998; 98US-0109100.
XX PA (IMMV) IMMUNEX CORP.
XX PI Graddis TJ, McGrew JT;
XX DR WPI; 2000-182115/16.
XX PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
XX PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
PS Claim 4; Page 85-86; 90pp; English.
XX CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAV69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the K64T mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX SQ Sequence 209 AA:
SQ
Query Match 89.2%; Score 1108; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.6e-96;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLWRLVLAQRMMERL 86
DB 1 tqdcsfqhpsissdfavkirelsdyllqdyptvasnldgeelcgglwrlvlaqrmmert 60
QY 87 KTYVAGSKMGGLLERVNTETHEVTKCAFQPPSCLRPVQTNISRLQETSEQLVALKPWIT 146
DB 61 ktvagskmgglervnteihfvtkcafpfpsscrlrfvqtnisrlqetseqvalkpwit 120
QY 147 RQNFSCLELQCCPDSSTLPPWSPRLATAPTAQPRLLLLLLLPVGLLLLLAAWCLH 206
DB 121 rqnfsclclqccpdssclppwsprrleataptapqppllllllpvgllllaaawclh 180
QY 207 WQTRRRTRPRGCVPPVPSPODLLVEH 235
DB 181 wqtrrrtrprgcvppvpspdqllllveh 209
RESULT 16
AAV69728
ID AAV69728 standard; Protein: 209 AA.
XX
AC AAV69728;
XX
XX 05-JUL-2000 (first entry)
XX
DE Huhnan flt-3 mutein L27P.

XX
KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX PN WO200001823-A2.
XX PD 13-JAN-2000.
XX PF 25-JUN-1999; 99WO-US14296.
XX PR 02-JUL-1998; 98US-0109100.
XX PA (IMMV) IMMUNEX CORP.
XX PI Graddis TJ, McGrew JT;
XX DR WPI; 2000-182115/16.
XX PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
XX PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
PS Claim 13; Page 83-84; 90pp; English.
XX CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the L27P mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX SQ Sequence 209 AA:
SQ
Query Match 89.1%; Score 1107; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.9e-96;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPTVASNLQDEELCGGLWRLVLAQRMMERL 86
DB 1 tqdcsfqhpsissdfavkirelsdyllqdyptvasnldgeelcgglwrlvlaqrmmert 60
QY 87 KTYVAGSKMGGLLERVNTETHEVTKCAFQPPSCLRPVQTNISRLQETSEQLVALKPWIT 146
DB 61 ktvagskmgglervnteihfvtkcafpfpsscrlrfvqtnisrlqetseqvalkpwit 120
QY 147 RQNFSCLELQCCPDSSTLPPWSPRLATAPTAQPRLLLLLLLPVGLLLLLAAWCLH 206
DB 121 rqnfsclclqccpdssclppwsprrleataptapqppllllllpvgllllaaawclh 180
QY 207 WQTRRRTRPRGCVPPVPSPODLLVEH 235
DB 181 wqtrrrtrprgcvppvpspdqllllveh 209

RESULT 17
AA69725
ID AAY69725 standard; Protein: 209 AA.
XX
AC AAY69725;
XX
DT 05-JUL-2000 (first entry)
XX
DE Human flt-3 mutein W18R.
XX
KW Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;
KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
KW cellular expansion; cellular differentiation; natural killer cell;
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
KW multiple myeloma; leukemia; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200001823-A2.
XX
PD 13-JAN-2000.
XX
PF 25-JUN-1999; 99WO-US14296.
XX
PR 02-JUL-1998; 98US-0109100.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Graddis TJ, McGrew JT;
XX
DR WPI: 2000-18215/16.
XX
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
PT immune response stimulation or treatment of pathological conditions
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
XX
PS Claim 4; Page 86-87; 90pp; English.
XX
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
CC which exhibits increased or decreased biological activity relative to
CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
CC polypeptides. This sequence represents an example of the novel flt-3
CC ligands and comprises the W18R mutant polypeptide. The flt3-L protein
CC binds cell surface tyrosine kinase receptors and regulate growth and
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
CC be used to induce cellular expansion (especially in vivo) or
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
CC cells, especially in the presence of growth factors such as interleukins,
CC colony stimulating factors or protein kinases. The protein can also
CC modulate, augment or enhance a patient's immune response and can be used
CC to treat an immune disorder (e.g. allergy, autoimmunity or
CC immunosuppression). The protein may be used to treat a pathological
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
CC myeloma, neuroblastoma or acute leukemia.
XX
XX
SQ Sequence 209 AA;
XX
Query Match 88.6%; Score 1100; DB 21; Length 209;
Best Local Similarity 99.5%; Pred. No. 8.8e-96;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TOPCSPOHSRTSSDFANKRELSDYLLQDPYVAVASLQDEELCGRLVLAQRMWERL 86
Db 1 tqdcstqhspsissdfavkirelsdyllqdyvtvasnlqdeecgglwtvlagymwrl 60
QY 87 KTVAGSKMGLLRVNTVEHFVTKCAFPQPPSCLRFVQTNISRLQETSQDLVALKPMWT 146
|||||

Db 61 ktvagskmqgllervntveihfvtkcafqpppsclrfvqtnisrllqetseq\valkprlt 120
QY 147 RQNFSEKLEIACQDPSSSTLPPWSPRPLEATAPAPOPLLDLLLPVGLLTAAMCLH 206
Db 121 rqnfsrclqgcqpsdstlpppwsprpleataptapqppllllllpvgllllaawclh 180
QY 207 WQTRRRTRPREQVPPVPSPODLLVEH 235
Db 181 wqtrrrtrpreqvyppvspqdlllveh 209
RESULT 18
AAB20195
ID AAB20195 standard; Protein: 185 AA.
XX
AC AAB20195;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human Flt-3 ligand (secreted form).
XX
KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..185
FT /label= Mature_protein
XX
PN WO200109303-A2.
XX
PD 08-FEB-2001.
XX
PF 31-JUL-2000; 2000WO-US20679.
XX
PR 30-JUL-1999; 99US-0146170.
XX
PA (VICA) VICAL INC.
XX
PI Hermanson GG;
XX
DR WPI: 2001-123319/13.
DR N-PSDB: AAF30312, AAF30314.
XX
PT Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
PS Claim 2; Page 138; 149pp; English.
XX
CC The present sequence is that of a secreted form of human Fms-like
CC tyrosine kinase (Flt-3 ligand), lacking the transmembrane and
CC cytoplasmic domains of the full-length form (see AAB20194). This
CC secreted form of the flt-3 ligand is expressed by vector VR6230
CC (see AAF30314). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a flt-3
CC ligand-encoding polynucleotide, such as VR6230, and 1 or more
CC antigen- or cytokine-encoding polynucleotides. The polynucleotides
CC are incorporated into the cells of the vertebrate in vivo, and a
CC prophylactically or therapeutically effective amount of flt-3
CC ligand and 1 or more antigens or cytokines is produced in vivo.
CC Pharmaceutical compositions comprising the polynucleotides are
CC useful for suppressing tumour growth in a mammal. The tumour is
CC melanoma, glioma or lymphoma, particularly B-cell lymphoma. The
CC claimed pharmaceutical compositions can also be used for the
CC prophylactic and/or therapeutic treatment of: (a) bacterial (e.g.
CC Bacillus infections), viral (e.g. hepatitis B and C in humans),

CC parasitic (e.g. malaria) and fungal infections; (b) autoimmune
 CC diseases (e.g. rheumatoid arthritis and osteoarthritis); (c)
 CC cancer; and (d) Aujeszky's disease in pigs. Various other examples
 CC of these diseases are given in the specification.

XX Sequence 185 AA:

Query Match 78.1%; Score 970; DB 22; Length 185;
 Best Local Similarity 99.5%; Pred. No. 1.4e-83;
 Matches 184; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGISGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
 Db 1 mtlvapawspctyYLLLLLLSSGISGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60

QY 61 ASNODEELCGGLNRVLAQRWMERLKTVAAGSKMOGLLEVRNTEIHVYTKCARQPPPSCL 120
 Db 61 asnldgeelcgglwrlvlaqrwmerlktvagskmqgllevrnteihvltkcarqpppscl 120

QY 121 RFVQNTISRLOETSEOLVALKPWITRONFSRCLELOCCPDSSSTLPPMSPRPLEATAPT 180
 Db 121 rfvgntisrllqetseqlvalkpwitrtqfsclelqcgpdssstlppmwsprpleatapt 180

QY 181 APQPP 185
 Db 181 apqpp 185

RESULT 19
 AAY58204
 ID AAY58204 standard; Protein; 294 AA.

AC AAY58204;
 DT 14-MAR-2000 (first entry)

XX Canine Flt-3 ligand.
 XX Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.
 XX WO9961618-A2.

PD 02-DEC-1999.
 XX

PF 28-MAY-1999; 99WO-US11942.
 XX

PR 29-MAY-1998; 98US-0087306.
 XX (HESK-) HESKA CORP.

PI Slim G, Yang S, Dreitz MJ, Wonderling RS;
 DR WPI; 2000-072623/06.
 DR N-PSDB; AAZ55487, AAZ55488, AAZ55489, AAZ55490.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 XX Claim 3b; Page 159-160; 264pp; English.

XX Sequences AAY58204 and AAY58206-Y58209 respectively represent
 CC encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while
 CC sequences AAY58210-Y58211 represent encoded and mature feline Flt-3
 CC ligand. The invention relates to canine interleukin-4 (IL-4),
 CC canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, and nucleotides associated

CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense
 CC oligonucleotides). The proteins may be used to raise antibodies and to
 CC screen for modulators of activity, while the antibodies may be used in
 CC detection, and in drug targeting.

XX Sequence 294 AA:

Query Match 72.1%; Score 895.5; DB 21; Length 294;
 Best Local Similarity 77.1%; Pred. No. 2.6e-76;
 Matches 182; Conservative 12; Mismatches 35; Indels 7; Gaps 3;

QY 1 MTVLAPAMSPPTYYLLLLLLSSGISGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
 Db 1 mtlvapawspctasLLLLLLSSGISGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60

QY 61 ASNODEELCGGLNRVLAQRWMERLKTVAAGSKMOGLLEVRNTEIHVYTKCARQPPPSCL 120
 Db 61 asnldgeelcgglwrlvlaqrwmerlktvagskmqgllevrnteihvltkcarqpppscl 120

QY 121 RFVQNTISRLOETSEOLVALKPWITRONFSRCLELOCCPDSSSTLPPMSPRPLEATAPT 180
 Db 121 rfvgntisrllqetseqlvalkpwitrtqfsclelqcgpdssstlppmwsprpleatapt 180

QY 181 APQPP-LLLLLLLPYGLLLAAAWCLHW-QRTRRTPRGQVPPVS----PQD 229
 Db 181 apqpprllllllpyalllmstawlhwrrrrrrrpygqrlrpsershlped 236

RESULT 20
 AAY58210
 ID AAY58210 standard; Protein; 291 AA.

AC AAY58210;
 DT 14-MAR-2000 (first entry)

XX Feline Flt-3 ligand.
 XX Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Felis catus.
 XX WO9961618-A2.

PD 02-DEC-1999.
 XX

PF 28-MAY-1999; 99WO-US11942.
 XX

PR 29-MAY-1998; 98US-0087306.
 XX (HESK-) HESKA CORP.

PI Slim G, Yang S, Dreitz MJ, Wonderling RS;
 DR WPI; 2000-072623/05.
 DR N-PSDB; AAZ55518, AAZ55519, AAZ55520, AAZ55521.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 XX Claim 3c; Page 186-187; 264pp; English.
 XX Sequences AAY58204 and AAY58206-Y58209 respectively represent


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RESULT 24
AA58211
ID AAY58211 standard; Protein; 265 AA.
XX
AC AAY58211;
XX
DT 14-MAR-2000 (first entry)
XX
DE Feline mature Flt-3 ligand.
XX
KW Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
KM immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Fels catus.
XX
PN WO961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR / 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Slim G, Yang S, Dreltz MJ, Wonderling RS;
XX
DR N-PSDB; AA55522, AA55523.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
PS Claim 3c: Page 191-192; 264pp; English.
XX
CC Sequences AAY58204 and AAY58206-Y58209 respectively represent
CC encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while
CC sequences AAY58210-Y58211 represent encoded and mature feline Flt-3
CC ligand. The invention relates to canine interleukin-4 (IL-4),
CC canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense
CC oligonucleotides). The proteins may be used to raise antibodies and to
CC screen for modulators of activity, while the antibodies may be used in
CC detection, and in drug targeting.
XX
SQ Sequence 265 AA;
XX
Query Match 63.7%; Score 791.5; DB 21; Length 265;
Best Local Similarity 80.8%; Pred. No. 1.5e-66;
Matches 156; Conservative 8; Mismatches 28; Indels 1; Gaps 1;
OY 29 DCSFQSPISDSFAVKIRELSDYLDQDYVTVASNLDELGGLMRVLQAQRMMERLKT 88
DB 3 dcsfshpslstkvtckrlrslsdyllqdyprvasnlgdelogpwhvlagrwmgrik 62
OY 89 VASGKQGLIERVNTIEHYTKAFOPPPSCRFVOTNISRLLQETSDEQVALAKWITR 148
DB 63 vagsqmsllaevnteihvylcaifpdlpsclrfvqtnishllgdtseqlaalkpwlttr 122
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OY 149 NFSRCLELOCQPDSSSTLPSPSPLEXTAPPAQPP-LLLLLLPYGLLLAAACLIHW 207
DB 123 nfsqclelqcqpdssstlpiprpspraleataalpqpaplllllllpallmsaawclhw 182
OY 208 ORTRRRTPRRGEQ 220
DB 183 rrrrrwrrpyreq 195
RESULT 25
AAR67540
ID AAR67540 standard; Protein; 231 AA.
XX
AC AAR67540;
XX
DT 05-AUG-1995 (first entry)
XX
DE Mouse flt-3 ligand.
XX
KW Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH Peptide 1..27
FH FT /label= Sig_peptide
FH FT 28..188
FH FT /label= Extracellular_domain
FH FT 189..211
FH FT /label= Transmembrane_domain
FH FT 212..231
FH FT /label= Cytoplasmic_domain
PN EP627487-A.
XX
PD 07-DEC-1994.
XX
PF 19-MAY-1994; 94EP-0303575.
XX
PR 24-MAY-1993; 93US-0068394.
PR 12-AUG-1993; 93US-0106463.
PR 25-AUG-1993; 93US-0111758.
PR 03-DEC-1993; 93US-0162407.
PR 07-MAR-1994; 94US-0209502.
PR 11-MAY-1994; 94US-0243545.
XX
PA (IMM) IMMUNEX CORP.
XX
PI Beckmann MP, Lyman SD;
XX
DR WPI; 1995-008071/02.
XX
DR N-PSDB; AAG79076.
XX
PT Isolated ligands for flt 3 receptors - useful for treating
PT anaemia, AIDS and various cancers
XX
PS Disclosure; Page 25-27; 33pp; English.
XX
CC cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a
CC cDNA library of T-cell line P7B-0.3A4 in CV-1/EBNA-1 cells
CC using a slide autoradiography method. Flt3-L stimulates
CC production of progenitor and stem cells, and can be used e.g.
CC in gene therapy protocols.
XX
SQ Sequence 231 AA;
XX
Query Match 61.9%; Score 768.5; DB 16; Length 231;
Best Local Similarity 70.3%; Pred. No. 1.9e-64;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
OY 1 MTVLAWMSP-FTYLLLLLSGLSGTODCSFQSPISDSFAVKIRELSDYLDQDYPT 59
||||| :: ||||| | || | ||||| || ||||| |||||
```

Tue Aug 6 09:34:29 2002

us-09-448-378-1.ray

Page 16

[illegible]

Search completed: August 6, 2002, 09:39:02
Job time: 293 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:37:59 ; Search time 201.6 Seconds

(without alignments)
410,295 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MYTLAPANSPTITLILLLL.....RREGQVPVPSPDILLVEH 235

Scoring table:

BLOSUM62
Gap: 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCRNUS.COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US05.COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07.COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080.COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081.COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082.COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US083.COMB.pep:*
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25: /cgn2_6/ptodata/2/paa/US102.COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US103.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	1	Sequence 4, Appl1
2	1242	100.0	235	5	Sequence 6, Appl1
3	1242	100.0	235	5	Sequence 6, Appl1
4	1242	100.0	235	5	Sequence 6, Appl1
5	1242	100.0	235	8	Sequence 6, Appl1
6	1242	100.0	235	8	Sequence 6, Appl1
7	1242	100.0	235	8	Sequence 6, Appl1

8	1242	100.0	235	10	US-08-669-692-6	Sequence 6, Appl1
9	1242	100.0	235	12	US-08-877-421-4	Sequence 4, Appl1
10	1242	100.0	235	18	US-09-448-378-1	Sequence 1, Appl1
11	1242	100.0	235	20	US-09-629-430B-19	Sequence 19, Appl1
12	1242	100.0	235	22	US-09-891-498-4	Sequence 4, Appl1
13	1242	100.0	235	23	US-09-904-536-1	Sequence 1, Appl1
14	1242	100.0	235	23	US-09-983-806-6	Sequence 6, Appl1
15	1242	100.0	235	24	US-10-095-449-6	Sequence 5, Appl1
16	1237	99.6	235	22	US-09-891-498-5	Sequence 34, Appl1
17	1236	99.5	235	5	US-08-155-111-34	Sequence 34, Appl1
18	1236	99.5	235	5	US-08-162-413-34	Sequence 34, Appl1
19	1236	99.5	235	6	US-08-261-553-34	Sequence 34, Appl1
20	1236	99.5	235	8	US-08-472-168-34	Sequence 34, Appl1
21	1236	99.5	235	8	US-08-484-882-34	Sequence 34, Appl1
22	1236	99.5	235	8	US-08-486-661-34	Sequence 34, Appl1
23	1236	99.5	235	20	US-09-629-430B-23	Sequence 23, Appl1
24	1124	90.5	212	23	US-09-904-536-10	Sequence 10, Appl1
25	1114	89.7	209	13	US-08-955-090-145	Sequence 145, Appl1
26	1114	89.7	209	23	US-09-904-536-18	Sequence 18, Appl1
27	1110	89.4	209	23	US-09-904-536-9	Sequence 9, Appl1
28	1110	89.4	209	23	US-09-904-536-12	Sequence 12, Appl1
29	1110	89.4	209	23	US-09-904-536-14	Sequence 14, Appl1
30	1110	89.4	209	23	US-09-904-536-17	Sequence 17, Appl1
31	1108	89.2	209	23	US-09-904-536-11	Sequence 11, Appl1
32	1108	89.2	209	23	US-09-904-536-15	Sequence 15, Appl1
33	1107	89.1	209	23	US-09-904-536-13	Sequence 13, Appl1
34	1106	89.0	209	23	US-09-904-536-8	Sequence 8, Appl1
35	1100	88.6	209	23	US-09-904-536-16	Sequence 16, Appl1
36	992	79.9	199	21	US-09-757-027-671	Sequence 671, Appl1
37	970	78.1	185	20	US-09-629-430B-24	Sequence 24, Appl1
38	963	77.5	189	22	US-09-891-498-2	Sequence 2, Appl1
39	895.5	72.1	294	17	US-09-322-409-7	Sequence 7, Appl1
40	895.5	72.1	294	18	US-09-451-527-7	Sequence 7, Appl1
41	894.5	72.0	291	17	US-09-322-409-44	Sequence 44, Appl1
42	894.5	72.0	291	18	US-09-451-527-44	Sequence 44, Appl1
43	834	67.1	178	20	US-09-629-430B-21	Sequence 21, Appl1
44	797.5	64.2	268	17	US-09-322-409-23	Sequence 23, Appl1
45	797.5	64.2	268	18	US-09-451-527-23	Sequence 23, Appl1
46	796.5	64.1	276	17	US-09-322-409-26	Sequence 26, Appl1
47	796.5	64.1	276	18	US-09-451-527-26	Sequence 26, Appl1
48	791.5	63.7	265	17	US-09-322-409-49	Sequence 49, Appl1
49	791.5	63.7	265	18	US-09-451-527-49	Sequence 49, Appl1
50	768.5	61.9	231	1	PCT-US98-12085-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1

Sequence 4, Application PCT/US9812085

GENERAL INFORMATION:

APPLICANT: IMMUNEX CORPORATION

TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM/PC Compatible

OPERATING SYSTEM: MS-DOS/Windows 95

SOFTWARE: Word for Windows 95, Version 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/12085

FILING DATE: 12-JUN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2855-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-us98-12085-4

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDFAVKIRLSYLLQDYPTV 60
DB 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDFAVKIRLSYLLQDYPTV 60
QY 61 ASNODEELCGLWRLVLAQRMMERLKTAVGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
DB 61 ASNODEELCGLWRLVLAQRMMERLKTAVGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSEQVLAQKFWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLQETSEQVLAQKFWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATPT 180
QY 181 APOPELLLLLPVGLLLAAACLIHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235
DB 181 APOPELLLLLPVGLLLAAACLIHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235

RESULT 2

US-08-106-463-6

Sequence 6, Application US/08106463

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/106,463

FILING DATE: 19930812

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-106-463-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDFAVKIRLSYLLQDYPTV 60
DB 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDFAVKIRLSYLLQDYPTV 60
QY 61 ASNODEELCGLWRLVLAQRMMERLKTAVGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
DB 61 ASNODEELCGLWRLVLAQRMMERLKTAVGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSEQVLAQKFWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATPT 180
DB 121 RFVQTNISRLQETSEQVLAQKFWITRQNFSCLELQCCPDSSSTLPPWSPRPLEATPT 180
QY 181 APOPELLLLLPVGLLLAAACLIHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235
DB 181 APOPELLLLLPVGLLLAAACLIHMQRTRRRTPRGEQVPVPSPQDLLLVEH 235

RESULT 3

US-08-111-758-6

Sequence 6, Application US/08111758

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.

APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen L. Malaska, Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: US

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0.1

SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/111,758

FILING DATE: August 25, 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-111-758-6

Query Match 100.0%; Score 1242; DB 5; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTYYLLLLSSGLSGTDCSPHSPISDFAVKIRELSYLLQDYPTV 60
DB 1 MTVALPAMSPPTYYLLLLSSGLSGTDCSPHSPISDFAVKIRELSYLLQDYPTV 60
QY 61 ASNLQDEELCGGLMRVLAQRMMERLKTVAAGSKMOGLERNTIHFVTKCAFQPPSCL 120
DB 61 ASNLQDEELCGGLMRVLAQRMMERLKTVAAGSKMOGLERNTIHFVTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APOPELLLLLPVGLLLAAAMCLHMORTRRRPPRGEQVPPVPSQDLLVEH 235
DB 181 APOPELLLLLPVGLLLAAAMCLHMORTRRRPPRGEQVPPVPSQDLLVEH 235

RESULT 4

US-08-162-407-6
; Sequence 6, Application US/08162407
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-407-6

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Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTVALPAMSPPTYYLLLLSSGLSGTDCSPHSPISDFAVKIRELSYLLQDYPTV 60

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DB 61 ASNLQDEELCGGLMRVLAQRMMERLKTVAAGSKMOGLERNTIHFVTKCAFQPPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180

DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPPMSPRPLEATAPT 180

QY 181 APOPELLLLLPVGLLLAAAMCLHMORTRRRPPRGEQVPPVPSQDLLVEH 235

DB 181 APOPELLLLLPVGLLLAAAMCLHMORTRRRPPRGEQVPPVPSQDLLVEH 235

RESULT 5

US-08-444-625-6
; Sequence 6, Application US/08444625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; City: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,625
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-625-6

Query Match 100.0%; Score 1242; DB 8; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
Db 1 MTVALPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
QY 61 ASNIQDEELCGGLMRLVLAQRMERLKVAGSKMGLERNTLHVTCAQPPSCL 120
Db 61 ASNIQDEELCGGLMRLVLAQRMERLKVAGSKMGLERNTLHVTCAQPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSKLELQCPDPSSTLPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSKLELQCPDPSSTLPWSPRPLEATAPT 180
QY 181 APOPPILLLLLPVGLLLAAACLMWQTRRRPRPEQVPPVPSFODLLVYH 235
Db 181 APOPPILLLLLPVGLLLAAACLMWQTRRRPRPEQVPPVPSFODLLVYH 235

RESULT 6

US-08-444-626-6
; Sequence 6, Application US/08444626

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; TITLE OF INVENTION: Ligands for fli3/fli-2 Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stephen L. Malaska, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.0.1

; SOFTWARE: Microsoft Word, Version #5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/444,626

; FILING DATE: 19-MAY-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/162,407

; FILING DATE: 03-DEC-1993

; APPLICATION NUMBER: 08/111,758

; FILING DATE: August 25, 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/106,463

; FILING DATE: August 12, 1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/068,394

; FILING DATE: May 24, 1993

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Malaska, Stephen L.

; REGISTRATION NUMBER: 32,655

; REFERENCE/DOCKET NUMBER: 2813-C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; TELEEX: 756822

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 235 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-444-626-6

Query Match 100.0%; Score 1242; DB 8; Length 235;

Best Local Similarity 100.0%; Pred. No. 2.6e-102; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0;

QY 1 MTVALPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
Db 1 MTVALPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDPAVKIRELSYLLQDYPVTV 60
QY 61 ASNIQDEELCGGLMRLVLAQRMERLKVAGSKMGLERNTLHVTCAQPPSCL 120
Db 61 ASNIQDEELCGGLMRLVLAQRMERLKVAGSKMGLERNTLHVTCAQPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSKLELQCPDPSSTLPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSKLELQCPDPSSTLPWSPRPLEATAPT 180
QY 181 APOPPILLLLLPVGLLLAAACLMWQTRRRPRPEQVPPVPSFODLLVYH 235
Db 181 APOPPILLLLLPVGLLLAAACLMWQTRRRPRPEQVPPVPSFODLLVYH 235

RESULT 7

US-08-444-632-6
; Sequence 6, Application US/08444632

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; TITLE OF INVENTION: Ligands for fli3/fli-2 Receptors

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stephen L. Malaska, Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.0.1

; SOFTWARE: Microsoft Word, Version #5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/444,632

; FILING DATE: 19-MAY-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/162,407

; FILING DATE: 03-DEC-1993

; APPLICATION NUMBER: 08/111,758

; FILING DATE: August 25, 1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/106,463

; FILING DATE: August 12, 1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/068,394

; FILING DATE: May 24, 1993

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Malaska, Stephen L.

; REGISTRATION NUMBER: 32,655

; REFERENCE/DOCKET NUMBER: 2813-C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; TELEEX: 756822

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 235 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-444-632-6

US-08-444-632-6

Query Match	100.0%;	Score 1242;	DB 8;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 2.6e-102;		
Matches 235; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MTVLA	PAMS	PPTTY	LLLLLLLL	SSG	ISG	QODCS	FOHSP	ISSPFAV	KIRLS	SYLL	LODYPV	60
QY	1	MTVLA	PAMS	PPTTY	LLLLLLLL	SSG	ISG	QODCS	FOHSP	ISSPFAV	KIRLS	SYLL	LODYPV	60
Db	1	MTVLA	PAMS	PPTTY	LLLLLLLL	SSG	ISG	QODCS	FOHSP	ISSPFAV	KIRLS	SYLL	LODYPV	60
QY	61	ASNLO	DEEL	CGGL	WRLV	LAO	RMR	ELKT	VAGSK	MOGLLE	RVNTE	HFHV	TCAC	QPPPSCL
Db	61	ASNLO	DEEL	CGGL	WRLV	LAO	RMR	ELKT	VAGSK	MOGLLE	RVNTE	HFHV	TCAC	QPPPSCL
QY	121	RFVOT	INIS	RLLQ	ETSE	BOV	VALK	PIWIT	QONF	SRCL	ELOC	QPD	SS	TLPP
QY	121	RFVOT	INIS	RLLQ	ETSE	BOV	VALK	PIWIT	QONF	SRCL	ELOC	QPD	SS	TLPP
Db	121	RFVOT	INIS	RLLQ	ETSE	BOV	VALK	PIWIT	QONF	SRCL	ELOC	QPD	SS	TLPP
QY	181	APOP	LLLL	LLLL	PG	GL	LL	LA	AMC	LH	QOR	RR	RR	PR
QY	181	APOP	LLLL	LLLL	PG	GL	LL	LA	AMC	LH	QOR	RR	RR	PR
Db	181	APOP	LLLL	LLLL	PG	GL	LL	LA	AMC	LH	QOR	RR	RR	PR

RESULT 8

US-08-669-692-6

sequence 6, Application US/08069692
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flk3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,692
FILING DATE: 24-JUN-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 7568822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-669-692-6

Query Match	100.0%;	Score 1242;	DB 10;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 2.6e-102;		
Matches 235; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MTVLAFAWSPPTYYLLLLLLLLSSGSLSGQDSCFQSPHSPSSDPFAKRLRESDYLDQPYTV	60
Db	1	MTVLAFAWSPPTYYLLLLLLLLSSGSLSGQDSCFQSPHSPSSDPFAKRLRESDYLDQPYTV	60
QY	61	ASNLODEBELCGGIMRLVLAQSMRMLKLTVAAGSKNOGILREVMTEIHFTVYKCAFQPPESCL	120
Db	61	ASNLODEBELCGGIMRLVLAQSMRMLKLTVAAGSKNOGILREVMTEIHFTVYKCAFQPPESCL	120
QY	121	RFVQVNIISRLLOETSEQVVALKPMWITRONFSRCLELQCPDSDTLPPEWSPRELEATAPT	180
Db	121	RFVQVNIISRLLOETSEQVVALKPMWITRONFSRCLELQCPDSDTLPPEWSPRELEATAPT	180
QY	181	APQPELLLLLLLTVGILLTAAAMCLMHQORRRPRPREGQVPPVPSQDILLVEH	240
Db	181	APQPELLLLLLLTVGILLTAAAMCLMHQORRRPRPREGQVPPVPSQDILLVEH	240

RESULT 9

US-08-877-421-4

```

1 Sequence 4, Application US/08877421
2 GENERAL INFORMATION:
3 APPLICANT: Viney, Joanne L.
4 APPLICANT: Mowatt, Allan M.
5 APPLICANT: Abbott, Nicholas
6 TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To
7 NUMBER OF SEQUENCES: 4
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Stephen L. Malaska, Immunex Corporation
10 STREET: 51 University Street
11 CITY: Seattle
12 STATE: Washington
13 COUNTRY: US
14 ZIP: 98101
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: Apple Power Macintosh
18 OPERATING SYSTEM: Macintosh 7.6
19 SOFTWARE: Microsoft Word, Version #6.0.1
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/877,421
22 FILING DATE: 17-JUN-1997
23 CLASSIFICATION: 514
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Malaska, Stephen L.
26 REGISTRATION NUMBER: 32,655
27 REFERENCE/DOCKET NUMBER: 2855
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (206) 587-0430
30 TELEFAX: (206) 233-0644
31 TELEX: 756822
32 INFORMATION FOR SEQ ID NO: 4:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 235 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37 MOLECULE TYPE: protein
38 US-08-877-421-4

```

Query Match	100.0%	Score 1242;	DB 12;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 2,6e-102;		
Matches 235;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps	0;
QY	1	MTVLAAPMSPTTYLLILLSSGISGTDCCSQHSPISDPAAVKIRLSYLLQDYPPVY	60	

```
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
QY 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
Db 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
QY 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235

RESULT 10
US-09-448-378-1
; Sequence 1, Application US/09448378
; GENERAL INFORMATION:
; APPLICANT: Brasel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-448-378-1

Query Match 100.0%; Score 1242; DB 18; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
QY 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
Db 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
QY 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235

RESULT 11
US-09-629-430B-19
; Sequence 19, Application US/09629430B
; GENERAL INFORMATION:
; APPLICANT: Hermanson, Gary George
; TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
; FILE REFERENCE: 1530.0130001
; CURRENT APPLICATION NUMBER: US/09/629,430B
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/146,170
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 235
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-629-430B-19
```

```
Query Match 100.0%; Score 1242; DB 20; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
QY 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
Db 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
QY 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235

RESULT 12
US-09-891-498-4
; Sequence 4, Application US/09891498
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: C1001244
; CURRENT APPLICATION NUMBER: US/09/891,498
; CURRENT FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRF
; ORGANISM: Human
US-09-891-498-4

Query Match 100.0%; Score 1242; DB 22; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
QY 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
Db 61 ASNIQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGGLEEVNTEIHFTVCARQPPPSCL 120
QY 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQDLVAKPWITRONFSRCLELQCPDSSSTLPPMSPRPLEATAPT 180
QY 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235
Db 181 APQPLLILLLLPVGLLLAAACLMHQRTRRRTPRPEQVPPVPSQDILLVEH 235

RESULT 13
US-09-904-536-1
; Sequence 1, Application US/09904536
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
```

CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-1

Query Match 100.0%; Score 1242; DB 23; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVLAPWSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
DB 1 MYVLAPWSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRLVLAQRMMERLKTIVAGSKMOGLIERVNTETIHFTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLMRLVLAQRMMERLKTIVAGSKMOGLIERVNTETIHFTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APQPELLLLLPVGLLLAAAMCLHMORTRRTPRPGQVPPVPSPODLLLVH 235
DB 181 APQPELLLLLPVGLLLAAAMCLHMORTRRTPRPGQVPPVPSPODLLLVH 235

RESULT 14
US-09-983-806-6
Sequence 6, Application US/09983806
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/983, 806
FILING DATE: 25-Oct-2001
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/444, 626
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: US 08/162, 407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111, 758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106, 463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068, 394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-983-806-6

Query Match 100.0%; Score 1242; DB 23; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-102;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVLAPWSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
DB 1 MYVLAPWSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSIDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRLVLAQRMMERLKTIVAGSKMOGLIERVNTETIHFTKCAFQPPPSCL 120
DB 61 ASNLQDEELCGGLMRLVLAQRMMERLKTIVAGSKMOGLIERVNTETIHFTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSKCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APQPELLLLLPVGLLLAAAMCLHMORTRRTPRPGQVPPVPSPODLLLVH 235
DB 181 APQPELLLLLPVGLLLAAAMCLHMORTRRTPRPGQVPPVPSPODLLLVH 235

RESULT 15
US-10-095-449-6
Sequence 6, Application US/10095449
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095, 449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669, 692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162, 407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111, 758
FILING DATE: August 25, 1993
APPLICATION NUMBER: 08/106, 463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068, 394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-095-449-6

Query Match

Best Local Similarity 100.0%; Score 1242; DB 24; Length 235;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MTVALPAMSPPTTYLLILLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
Db 1 MTVALPAMSPPTTYLLILLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNLQDELGGLMRVLVAQRMERLKTVAAGSMOGLERVTETHEFTKCAFOPPPSCL 120
Db 61 ASNLQDELGGLMRVLVAQRMERLKTVAAGSMOGLERVTETHEFTKCAFOPPPSCL 120
QY 121 REVQTNISRLQETSQDLVALKPKWITRONFSRCLQLCOCPDSSSTLPPEWSPPLEATAPT 180
Db 121 REVQTNISRLQETSQDLVALKPKWITRONFSRCLQLCOCPDSSSTLPPEWSPPLEATAPT 180
QY 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRPGQVPPVPSPODLLLVEH 235
Db 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRPGQVPPVPSPODLLLVEH 235
```

RESULT 16

US-09-891-498-5

Sequence 5, Application US/09891498

GENERAL INFORMATION:

APPLICANT: GONG, Fangcheng et al.

TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

TITLE OF INVENTION: USFS THEREOF

FILE REFERENCE: CLO01244

CURRENT APPLICATION NUMBER: US/09/891,498

CURRENT FILING DATE: 2001-06-27

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 235

TYPE: PROT

ORGANISM: Human

US-09-891-498-5

Query Match

Best Local Similarity 99.6%; Score 1237; DB 22; Length 235;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MTVALPAMSPPTTYLLILLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
Db 1 MTVALPAMSPPTTYLLILLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNLQDELGGLMRVLVAQRMERLKTVAAGSMOGLERVTETHEFTKCAFOPPPSCL 120
Db 61 ASNLQDELGGLMRVLVAQRMERLKTVAAGSMOGLERVTETHEFTKCAFOPPPSCL 120
QY 121 REVQTNISRLQETSQDLVALKPKWITRONFSRCLQLCOCPDSSSTLPPEWSPPLEATAPT 180
Db 121 REVQTNISRLQETSQDLVALKPKWITRONFSRCLQLCOCPDSSSTLPPEWSPPLEATAPT 180
QY 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRPGQVPPVPSPODLLLVEH 235
Db 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRPGQVPPVPSPODLLLVEH 235
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Db 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 17

US-08-155-111-34

Sequence 34, Application US/08155111

GENERAL INFORMATION:

APPLICANT: Hannum, Charles H.

APPLICANT: Culpepper, Janice A.

APPLICANT: Lee, Frank D.

APPLICANT: Birnbaum, Daniel

TITLE OF INVENTION: Purified Mammalian Flt3 Ligands;

TITLE OF INVENTION: Agonists; Antagonists

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESS: DNA Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/155,111

FILING DATE: 19-NOV-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0350K4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-155-111-34

Query Match

Best Local Similarity 99.5%; Score 1236; DB 5; Length 235;

Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 MTVALPAMSPPTTYLLILLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
Db 1 MTVALPAMSPPTTYLLILLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLDDYPTV 60
QY 61 ASNLQDELGGLMRVLVAQRMERLKTVAAGSMOGLERVTETHEFTKCAFOPPPSCL 120
Db 61 ASNLQDELGGLMRVLVAQRMERLKTVAAGSMOGLERVTETHEFTKCAFOPPPSCL 120
QY 121 REVQTNISRLQETSQDLVALKPKWITRONFSRCLQLCOCPDSSSTLPPEWSPPLEATAPT 180
Db 121 REVQTNISRLQETSQDLVALKPKWITRONFSRCLQLCOCPDSSSTLPPEWSPPLEATAPT 180
QY 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRPGQVPPVPSPODLLLVEH 235
Db 181 APOPELILLLLPYGILLLLAAACLMHQRTRRRTPRPGQVPPVPSPODLLLVEH 235
```

RESULT 18

US-08-162-413-34

Sequence 34, Application US/08162413

GENERAL INFORMATION:

APPLICANT: Hannum, Charles H.

APPLICANT: Culpepper, Janice A.

APPLICANT: Lee, Frank D.
TITLE OF INVENTION: Purified Mammalian Flt3 Ligands;
TITLE OF INVENTION: Agonists; Antagonists
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,413
FILING DATE: 03-DEC-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-413-34

Query Match 99.5%; Score 1236; DB 5; Length 235;
Best Local Similarity 99.6%; Pred. No. 9,1e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLA PAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
DB 1 MTVLA PAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNLODEBELCGALMRLVLAQRMMERLKTVA GSKMGLLERYNTEIHVFYKCAFPSPSCL 120
DB 61 ASNLODEBELCGALMRLVLAQRMMERLKTVA GSKMGLLERYNTEIHVFYKCAFPSPSCL 120
QY 121 RFVQVNIISRLQETSEQLVALKFWITRONFSRCLFQCPDSSSTLPPMPSPRLEATAPT 180
DB 121 RFVQVNIISRLQETSEQLVALKFWITRONFSRCLFQCPDSSSTLPPMPSPRLEATAPT 180
QY 181 APOPELLLLLLLVGLLLAAAWCLMORTRRTPRPGGOVPPVPSQDLLVEH 235
DB 181 APOPELLLLLLLVGLLLAAAWCLMORTRRTPRPGGOVPPVPSQDLLVEH 235

RESULT 19
US-08-261-553-34
Sequence 34, Application US/08261553
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
TITLE OF INVENTION: AGONISTS; ANTAGONISTS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,553
FILING DATE: 17-JUN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-261-553-34

Query Match 99.5%; Score 1236; DB 6; Length 235;
Best Local Similarity 99.6%; Pred. No. 9,1e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLA PAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
DB 1 MTVLA PAMSPPTTYLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYPTV 60
QY 61 ASNLODEBELCGALMRLVLAQRMMERLKTVA GSKMGLLERYNTEIHVFYKCAFPSPSCL 120
DB 61 ASNLODEBELCGALMRLVLAQRMMERLKTVA GSKMGLLERYNTEIHVFYKCAFPSPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCQPPSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCQPPSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLILLLIPVGLLLLAAMCLHWQRTTRRRPRPEQVPPVSPQDLLVEH 235
Db 181 APQPLLILLLIPVGLLLLAAMCLHWQRTTRRRPRPEQVPPVSPQDLLVEH 235

RESULT 20

US-08-472-168-34
Sequence 34, Application US/08472168
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
APPLICANT: Birnbaum, Daniel
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
TITLE OF INVENTION: AGONISTS; ANTAGONISTS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,168
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,553
FILING DATE: 17-JUN-1994
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9156
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-168-34

Query Match

99.5%; Score 1236; DB 8; Length 235;

Best Local Similarity 99.6%; Pred. No. 9,1e-102;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSLGTDGCSROHSPISSDPAVKIRRELSYLLDDYPTV 60
Db 1 MTVLAPAMSPPTTYLLLLSSGSLGTDGCSROHSPISSDPAVKIRRELSYLLDDYPTV 60
QY 61 ASNLQDEELCGALNRLVLAQRMERLKTIVAGSKMGLLEERYNTLHFYTKCAFQPPSCL 120
Db 61 ASNLQDEELCGALNRLVLAQRMERLKTIVAGSKMGLLEERYNTLHFYTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCQPPSSSTLPPWSPRPLEATAPT 180
Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLCQPPSSSTLPPWSPRPLEATAPT 180
QY 181 APQPLLILLLIPVGLLLLAAMCLHWQRTTRRRPRPEQVPPVSPQDLLVEH 235
Db 181 APQPLLILLLIPVGLLLLAAMCLHWQRTTRRRPRPEQVPPVSPQDLLVEH 235

RESULT 21

US-08-484-882-34
Sequence 34, Application US/08484882
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
APPLICANT: Birnbaum, Daniel
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
TITLE OF INVENTION: AGONISTS; ANTAGONISTS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,553
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K7GD
TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-486-882-34

Query Match 99.5%; Score 1236; DB 8; Length 235;
 Best Local Similarity 99.6%; Pred. No. 9.1e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLILLSSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPYTV 60
 DB 1 MTVLAPAMSPPTTYLLILLSSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPYTV 60
 QY 61 ASNQDEELGGLMRVLAQRMERLKTAVAGSKMGGLLERVNTIHFVTKCAFQPPPSCL 120
 DB 61 ASNQDEELGGLMRVLAQRMERLKTAVAGSKMGGLLERVNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 QY 181 APOPELLLLLLPVGLLLAAAMCLHWQRTRRPRRGEQVPVPSPODLLLVEH 235
 DB 181 APOPELLLLLLPVGLLLAAAMCLHWQRTRRPRRGEQVPVPSPODLLLVEH 235

RESULT 22
 US-08-486-661-34
 ; Sequence 34, Application US/08486661
 ; GENERAL INFORMATION:
 ; APPLICANT: Hannum, Charles H.
 ; APPLICANT: Culpepper, Janice A.
 ; APPLICANT: Lee, Frank D.
 ; APPLICANT: Birnbaum, Daniel
 ; TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
 ; TITLE OF INVENTION: AGONISTS; ANTAGONISTS
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,661
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-852-9196
 ; TELEFAX: 415-496-1200
 ; INFORMATION FOR SEQ ID NO: 34:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 235 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-486-661-34

Query Match 99.5%; Score 1236; DB 8; Length 235;
 Best Local Similarity 99.6%; Pred. No. 9.1e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLILLSSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPYTV 60
 DB 1 MTVLAPAMSPPTTYLLILLSSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPYTV 60
 QY 61 ASNQDEELGGLMRVLAQRMERLKTAVAGSKMGGLLERVNTIHFVTKCAFQPPPSCL 120
 DB 61 ASNQDEELGGLMRVLAQRMERLKTAVAGSKMGGLLERVNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 QY 181 APOPELLLLLLPVGLLLAAAMCLHWQRTRRPRRGEQVPVPSPODLLLVEH 235
 DB 181 APOPELLLLLLPVGLLLAAAMCLHWQRTRRPRRGEQVPVPSPODLLLVEH 235

RESULT 23
 US-09-629-430B-23
 ; Sequence 23, Application US/09629430B
 ; GENERAL INFORMATION:
 ; APPLICANT: Hermanson, Gary George
 ; TITLE OF INVENTION: FLT-3-ligand-Encoding Polynucleotide as a
 ; TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer
 ; FILE REFERENCE: 1530.0130001
 ; CURRENT APPLICATION NUMBER: US/09/629,430B
 ; CURRENT FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: 60/146,170
 ; PRIOR FILING DATE: 1999-07-30
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-629-430B-23

Query Match 99.5%; Score 1236; DB 20; Length 235;
 Best Local Similarity 99.6%; Pred. No. 9.1e-102;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLILLSSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPYTV 60
 DB 1 MTVLAPAMSPPTTYLLILLSSGLSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPYTV 60
 QY 61 ASNQDEELGGLMRVLAQRMERLKTAVAGSKMGGLLERVNTIHFVTKCAFQPPPSCL 120
 DB 61 ASNQDEELGGLMRVLAQRMERLKTAVAGSKMGGLLERVNTIHFVTKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRQNSRCLELQCPDPSSTLPPWSPRPLEATAPT 180
 QY 181 APOPELLLLLLPVGLLLAAAMCLHWQRTRRPRRGEQVPVPSPODLLLVEH 235
 DB 181 APOPELLLLLLPVGLLLAAAMCLHWQRTRRPRRGEQVPVPSPODLLLVEH 235

RESULT 24
 US-09-904-536-10
 ; Sequence 10, Application US/09904536
 ; GENERAL INFORMATION:
 ; APPLICANT: Gradalis, Thomas J.
 ; APPLICANT: McGrew, Jeffrey T.
 ; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
 ; FILE REFERENCE: 03260.0028

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: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
: LENGTH: 212
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-904-536-10

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	Query Match	90.5%	Score 1124	DB 23	Length 212
	Best Local Similarity	100.0%	Prod. No. 8,1e-92		
	Matches 211	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	25	SGTODCSFOHSPISDSPAFAVKIRELSDYLLDQYPVTVASNLQDEELCGGLRWLYLAQRWME	84		
Db	2	SGTODCSFOHSPISDSPAFAVKIRELSDYLLDQYPVTVASNLQDEELCGGLRWLYLAQRWME	61		
QY	85	RKTVAGSKMOGLEGLEVNTEIHFTVKCAQAPPSCGLRVPQNTSRLLQETSEQLVAIKPKP	144		
Db	62	RKTVAGSKMOGLEGLEVNTEIHFTVKCAQAPPSCGLRVPQNTSRLLQETSEQLVAIKPKP	121		
QY	145	ITRONFSRCLTELQCPDSDSTLPPPPSPRPLEATAFAPQPLLLLLLVGLLLAAAMC	204		
Db	122	ITRONFSRCLTELQCPDSDSTLPPPPSPRPLEATAFAPQPLLLLLLVGLLLAAAMC	181		
QY	205	LHMQRTRRRTRPRGEOVPPVPSQDLLVEH	235		
Db	182	LHMQRTRRRTRPRGEOVPPVPSQDLLVEH	212		

RESULT 25
US-08-955-090-145
Sequence 145, Application US/08955090
GENERAL INFORMATION:
APPLICANT: Mc Wether, Charles
APPLICANT: Feng, Yiqing
APPLICANT: Mc Keam, John
APPLICANT: Staten, Nicholas
APPLICANT: Streeter, Phillip
APPLICANT: Woulfe, Susan
APPLICANT: Minster, Nancy
APPLICANT: Minerly, John
TITLE OF INVENTION: Novel flt3 Receptor Agonists
NUMBER OF SEQUENCES: 151
CORRESPONDENCE ADDRESS:
ADDRESSEE: G. D. Searle Corporate Patent Department
STREET: P.O. Box 55110
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastsoft for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,090
FILING DATE: 21-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,094
FILING DATE: 25-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2993/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-737-6986

```

1 TELEFAX: 314-737-6972
2
3 TELE:
4
5 INFORMATION FOR SEQ ID NO: 145
6
7 SEQUENCE CHARACTERISTICS:
8
9 LENGTH: 209 amino acids
10
11 TYPE: amino acid
12
13 STRANDEDNESS: single
14
15 TOPOLOGY: linear
16
17 MOLECULE TYPE: None
18
19 OS-08-935-090-145

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Search completed: August 6, 2002, 09:44:48
Job time: 409 sec
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Tue Aug 6 09:34:31 2002

us-09-448-378-1.rapm

Page 13

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:37:29 ; Search time 38.79 Seconds
(without alignments)
914.856 Million cell updates/sec

Title:	US-09-448-378-1
Perfect score:	1242
Sequence:	1 MVTLPANSPPTVYLLILL...RPGQVPVPYSPQDLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 463719 seqs, 151009603 residues

Total number of hits satisfying chosen parameters: 463719

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries
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2: /c9n2.6/p/odata/1/paa/US06_NEW_COMB pep: *
3: /c9n2.6/p/odata/1/paa/US07_NEW_COMB pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1242	100.0	235	1	PCT-US02-20172-4	Sequence 4, App11
2	1242	100.0	235	7	US-60-368-263-1	Sequence 1, App11
3	1237	99.6	235	1	PCT-US02-20172-5	Sequence 5, App11
4	963	77.5	189	1	PCT-US02-20172-2	Sequence 2, App12
5	822	66.2	156	6	US-10-053-555A-1	Sequence 1, App11
6	768.5	61.9	231	7	US-60-368-263-2	Sequence 2, App11
7	97	7.8	637	7	US-60-391-781-1122	Sequence 1122, App11
8	95.5	7.7	671	5	US-09-935-625-5799	Sequence 5799, App11
9	93.5	7.5	658	7	US-60-382-098-359	Sequence 359, App11
10	92	7.4	251	5	US-09-629-469A-13654	Sequence 13654, App11
11	89.5	7.2	474	7	US-60-360-039-6104	Sequence 6104, App11
12	89.5	7.2	941	7	US-60-389-987-2466	Sequence 2466, App11
13	89	7.2	303	6	US-10-032-214-64	Sequence 64, App11
14	89	7.2	303	6	US-10-032-214-198	Sequence 198, App11
15	88.5	7.1	579	1	PCT-US02-21694-15	Sequence 15, App11
16	88.5	7.1	612	6	US-10-155-881-31529	Sequence 31529, App11
17	88.5	7.1	834	6	US-10-155-881-7333	Sequence 7333, App11
18	88.5	7.1	1257	6	US-10-109-924-2	Sequence 2, App11
19	88	7.1	238	6	US-10-174-363-30	Sequence 30, App11
20	87.5	7.0	239	6	US-10-155-881-21398	Sequence 21398, App11
21	87.5	7.0	300	6	US-10-032-214-207	Sequence 207, App11
22	87.5	7.0	479	6	US-10-108-605-57	Sequence 57, App11
23	87.5	7.0	570	1	PCT-US02-17598-104	Sequence 104, App11
24	87	7.0	303	6	US-10-032-214-174	Sequence 174, App11
25	87	7.0	303	6	US-10-032-214-177	Sequence 177, App11
26	87	7.0	597	5	US-09-746-311A-381	Sequence 381, App11

27	86	6.9	303	6	US-10-032-214-67	Sequence 67, App
28	86	6.9	303	6	US-10-032-214-206	Sequence 206, App
29	86	6.9	462	6	US-10-155-881-31551	Sequence 31551, A
30	86	6.9	677	6	US-10-155-881-7340	Sequence 7340, Ap
31	86	6.9	789	6	US-10-179-131-5768	Sequence 5768, Ap
32	86	6.9	1077	6	US-10-104-047-2291	Sequence 2291, Ap
33	85	6.8	282	5	US-09-629-469A-18922	Sequence 18922, A
34	85	6.8	303	6	US-10-032-214-186	Sequence 18922, A
35	85	6.8	1191	7	US-60-389-987-2063	Sequence 2063, App
36	84	6.8	220	1	PCT-US02-06388-2	Sequence 2, Appl
37	84	6.8	303	6	US-10-032-214-55	Sequence 55, Appl
38	84	6.8	687	5	US-09-629-469A-17435	Sequence 17435, A
39	84	6.8	1252	6	US-10-047-542-89	Sequence 89, Appl
40	83.5	6.7	335	7	US-60-360-039-4053	Sequence 4053, App
41	83.5	6.7	303	6	US-10-155-881-7832	Sequence 7832, Ap
42	83	6.7	303	6	US-10-032-214-51	Sequence 51, Appl
43	83	6.7	303	6	US-10-032-214-61	Sequence 61, Appl
44	83	6.7	303	6	US-10-032-214-66	Sequence 66, Appl
45	83	6.7	303	6	US-10-032-214-178	Sequence 178, App
46	83	6.7	303	6	US-10-032-214-185	Sequence 185, App
47	83	6.7	303	6	US-10-032-214-193	Sequence 193, App
48	83	6.7	303	6	US-10-032-214-197	Sequence 197, App
49	83	6.7	303	6	US-10-032-214-215	Sequence 215, App
50	83	6.7	303	6	US-10-032-214-220	Sequence 220, App

ALIGNMENTS

```

RESULT      1
PCT-US02-20172-4
; Sequence 4, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEIN,
; TITLE OF INVENTION: NOLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-4

```

Query Match	100.0%;	Score 1242;	DB 1;	Length 235;
Best Local Similarity	100.0%;	Pred. No. 5.5e-98;		
Matches 235;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MTVLAPAMSPPTYLLLLLLLLSSGLSGTODCSFQHSPISSDFAVKIKRELSDYLQDYEPVY	60	
Db	1	MTVLAPAMSPPTYLLLLLLLLSSGLSGTQDCSPQHSPISSDFAVKIKRELSDYLQDYEPVY	60	
QY				
QY	61	ASNLODEELCGGLMRVLAQRMMERIKTYAGSKMGGLERNTETHTFYTKARPPPSCL	120	
Db	61	ASNLODEELCGGLMRVLAQRMMERIKTYAGSKMGGLERNTETHTFYTKARPPPSCL	120	
QY				
QY	121	RFVQNTISRLLQETSEOLVALKFWITRQNFSCLELCQDOPSSSTLPWPMSRPLEAPPT	180	
Db	121	RFVQNTISRLLQETSEOLVALKFWITRQNFSCLELCQDOPSSSTLPWPMSRPLEAPPT	180	
QY				
QY	181	APQPELLLLLLLTVGLLLAAAMCCHWQTRRRTRPRGEOQVPVPPSPQDILLVEH	235	
Db	181	APQPELLLLLLLTVGLLLAAAMCCHWQTRRRTRPRGEOQVPVPPSPQDILLVEH	235	
RESULT	2			
US-60-368-263-1				
i Sequence 1, Application US/60368263				

```
; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368,263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-368-263-1

Query Match          100.0%; Score 1242; DB 7; Length 235;
Best Local Similarity 100.0%; Pred. No. 5,5e-98;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
DB 1 MTVLAPAMSPPTTYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLODEELCGGLMRVLVAQRMMERLKTVAAGSKMOGLLEEVNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLODEELCGGLMRVLVAQRMMERLKTVAAGSKMOGLLEEVNTEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCQDPSSTLPPMSPRPLEATAP 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCQDPSSTLPPMSPRPLEATAP 180
QY 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSPODLLLVEH 235
DB 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 3
PCT-US02-20172-5
; Sequence 5, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-5

Query Match          99.6%; Score 1237; DB 1; Length 235;
Best Local Similarity 99.6%; Pred. No. 1,5e-97;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
DB 1 MTVLAPAMSPPTTYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLODEELCGGLMRVLVAQRMMERLKTVAAGSKMOGLLEEVNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLODEELCGGLMRVLVAQRMMERLKTVAAGSKMOGLLEEVNTEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCQDPSSTLPPMSPRPLEATAP 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCQDPSSTLPPMSPRPLEATAP 180
```

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QY 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSPODLLLVEH 235
DB 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 4
PCT-US02-20172-2
; Sequence 2, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-2

Query Match          77.5%; Score 963; DB 1; Length 189;
Best Local Similarity 80.4%; Pred. No. 2,3e-74;
Matches 189; Conservative 0; Mismatches 0; Indels 46; Gaps 1;

QY 1 MTVLAPAMSPPTTYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
DB 1 MTVLAPAMSPPTTYLLLLLLLLSSGSGTQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTV 60
QY 61 ASNLODEELCGGLMRVLVAQRMMERLKTVAAGSKMOGLLEEVNTEIHFVTKCAFQPPPSCL 120
DB 61 ASNLODEELCGGLMRVLVAQRMMERLKTVAAGSKMOGLLEEVNTEIHFVTKCAFQPPPSCL 120
QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCQDPSSTLPPMSPRPLEATAP 180
DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLCLOCQDPSSTLPPMSPRPLEATAP 180
QY 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSPODLLLVEH 235
DB 181 APQPLLILLPLVGLLLAAACLMQRTRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 5
US-10-053-355A-1
; Sequence 1, Application US/10053355A
; GENERAL INFORMATION:
; APPLICANT: Rossi, Alex
; TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High
; TITLE OF INVENTION: Small Molecule Drug Discovery
; FILE REFERENCE: A-70882/RMS/AMS
; CURRENT APPLICATION NUMBER: US/10/053,355A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/316,723
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-355A-1

Query Match          66.2%; Score 822; DB 6; Length 156;
Best Local Similarity 100.0%; Pred. No. 1,8e-62;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDPAVKIRELSDYLLQDYPVTVASNLODEELCGGLMRVLVAQRMMERL 86
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4
Db 2 TDDCSFHSPLSDPAVAKIRELSDYLLDDYVAVASNLQDELCGLMRLVLAORMMERL 61
Qy 87 KTVAGSKMOGLIERVNTIEHFVTKCAFOPPPSCLEFVOTINSRLLQETSQOLVALKPWIT 146
Db 62 KTVASKNQGLIERVNTIEHFVTKCAFOPPPSCLEFVOTINSRLLQETSQOLVALKPWIT 121
Qy 147 RONSRCLELQCCPDSTLPPPMSPLEATAPTA 181
Db 122 RONSRCLELQCCPDSTLPPPMSPLEATAPTA 156

RESULT 6
US-60-368-263-2
; Sequence 2, Application US/60368263
; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Majiszwski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368,263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp
US-60-368-263-2

Query Match 61.9%; Score 768.5; DB 7; Length 231;
Best Local Similarity 70.3%; Pred. No. 1e-57;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

Qy 1 MTVALPAMSP-TTYLTLSSLSSTQCCSHSPSSIDDFAVKIRELSDYLLQDYPVT 59
Db 1 MTVALPAMSPSSLLTLTLSPCLRTGTPDCYSHSPSSISNFVKFRELTDHLKDYPTV 60
Qy 60 VASNLQDELCGLMRLVLAORMMERLKTVAAGSKMOGLIERVNTIEHFVTKCAFOPPPSC 119
Db 61 VAVNLQDEKCKKAMSLFLAQRWTEQAKTYAGSKMOGLIEDVNTIEHFVTSCTFQPLPEC 120
Qy 120 LRFQVNTISRLQETSQOLVALKPWITR--QNSRCLELQCCPDSTLPPPMSPLEAT 177
Db 121 LRFQVNTISRLQETSQOLVALKPWITR--QNSRCLELQCCPDSTLPPPMSPLEAT 180
Qy 178 APRAPOPP--LLLLLPVGLLLLAAMCQHMQRTRRTRRPRGEQVPPVSP 227
Db 181 ELPPRRPRLLLLLPLTLVLLAAMGLRMQRRARR--GELHFGVPLP 228

RESULT 7
US-60-391-781-1122
; Sequence 1122, Application US/60391781
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C.
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Oil in Plants
; FILE REFERENCE: 38-77(52900)B
; CURRENT APPLICATION NUMBER: US/60/391,781
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/365,301
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 3034
; SEQ ID NO 1122
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(637)
; OTHER INFORMATION: unsure at all Xaa locations
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US-60-391-781-1122
Query Match 7.8%; Score 97; DB 7; Length 637;
Best Local Similarity 32.9%; Pred. No. 4.4;
Matches 28; Conservative 8; Mismatches 25; Indels 24; Gaps 4;

Qy 162 SSTLPMPWSPRPLEATAPTA-PQPPILLLLLPVGLLLAA-----WCLHWQRTRRRT 214
Db 16 STSPPPWSPASLQATASASRPP-----PPGTTSSATATPTPRWPLRPSASVSRA 68
Qy 215 PRPEQVPP-----VPSPOD 229
Db 69 TSPGHCLPLPRAASAAAANVPAPCD 93
```

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RESULT 8
US-09-935-625-5799
; Sequence 5799, Application US/09935625
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
; FILE REFERENCE: 2750-1481P
; CURRENT APPLICATION NUMBER: US/09/935,625
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 33136
; SEQ ID NO 5799
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..671
; OTHER INFORMATION: Ceres Seq. ID no. 3071413
US-09-935-625-5799
```

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Query Match 7.7%; Score 95.5; DB 5; Length 671;
Best Local Similarity 27.7%; Pred. No. 6.4;
Matches 31; Conservative 14; Mismatches 28; Indels 39; Gaps 5;

Qy 138 LVALKRWITRQNSRCLEL---QCQPD-----SSTLPMPWSPR 172
Db 195 LVQCQPDRLRQCCSCQLQVNIQPTDRIGARIINPSCTSREIYAFTEBNAVPP--PP 252
Qy 173 PLEATAPTAPOP-----LLLLLP--VGLLLAAMCQHMQRTRR 212
Db 253 PPSISTPPVSAAPRSGKDGNSKVLVIAIVPITVAVLLFIAGYCFLTRARRK 304
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RESULT 9
US-60-382-898-359
; Sequence 359, Application US/60382898
; GENERAL INFORMATION:
; APPLICANT: Hudson, Keith
; APPLICANT: et al.
; TITLE OF INVENTION: Plant Receptors and Ligands
; FILE REFERENCE: 1066P
; CURRENT APPLICATION NUMBER: US/60/382,898
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 1344
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(658)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-382-898-359
```


US-60-389-987-2466

Query Match 7.2%; Score 89.5; DB 7; Length 941;
Best Local Similarity 44.1%; Pred. No. 31;
Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;

OY 170 SPRPLEATAPAPQPPLLL-LLLLLPVGLLLAAAMCLHMORTRRRTPRPGQPPV 224
DB 3 SPRSSGQPPPPPPPPARLLLLPLLPAGAW--GM---ARGAPRPPSSPPL 56

RESULT 13

US-10-032-214-64
; Sequence 64, Application US/10032214
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; APPLICANT: LAZETIC, ALEXANDRA
; APPLICANT: LEONG, STEVEN R.
; APPLICANT: CHANG, CHIA-CHUN
; APPLICANT: APT, DORIS
; APPLICANT: GUSTAFSSON, CLAES
; TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
; FILE REFERENCE: 02-106730US
; CURRENT APPLICATION NUMBER: US/10/032,214
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 09/888,324
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19973
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,946
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/241,245
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-032-214-64

Query Match 7.2%; Score 89; DB 6; Length 303;
Best Local Similarity 22.3%; Pred. No. 8.6;
Matches 35; Conservative 37; Mismatches 63; Indels 92; Gaps 17;

OY 15 LLLLLSSGLSGTQDSCFQHSPISSDFAVKIRELSDYLQ---DYPVYASMLQDEE--- 68
DB 103 IYLAIRLSDSGTYTCVIOKPVKLG--AYKLEHLASVRIMIRADPEVPTINDGNPSPNI 160
OY 69 ---LC---GGLMRVLAQRMME-----RLKTVAGSKMOGLERVNTETIHF-VTK----- 110
DB 161 RLICSTSGGFEPPRLA--WMEDGEELNNAVNTVDDDLTELXSVSSLEDFVNTGNHSTIV 218
OY 111 CAFQPPPSCLRFVQTNISRLQETSEQLVALKWPITRONFSRCLQLQCPDSDSTLPPWS 170
DB 219 C-----LTKYGELSVSQIF-----PWS 235
OY 171 PRPLEATAPAPQPPLLL-LLLPV-GILLILAA--WCL-----HMORTRRRTPRPG 218
DB 236 -KPKQ-----EPIIDLPEFWIITPVSGALVLTAVVLYCLACRHVARMKRRRNEETVG 287
OY 219 -EQVPPV 224
DB 288 TERLSPI 294

RESULT 14
US-10-032-214-198

; Sequence 198, Application US/10032214

; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; APPLICANT: LAZETIC, ALEXANDRA
; APPLICANT: LEONG, STEVEN R.
; APPLICANT: CHANG, CHIA-CHUN
; APPLICANT: APT, DORIS
; APPLICANT: GUSTAFSSON, CLAES
; TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
; FILE REFERENCE: 02-106730US
; CURRENT APPLICATION NUMBER: US/10/032,214
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 09/888,324
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19973
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,946
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/241,245
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-032-214-198

Query Match 7.2%; Score 89; DB 6; Length 303;
Best Local Similarity 22.3%; Pred. No. 8.6;
Matches 35; Conservative 37; Mismatches 63; Indels 92; Gaps 17;

OY 15 LLLLLSSGLSGTQDSCFQHSPISSDFAVKIRELSDYLQ---DYPVYASMLQDEE--- 68
DB 103 IYLAIRLSDSGTYTCVIOKPVKLG--AYKLEHLASVRIMIRADPEVPTINDGNPSPNI 160
OY 69 ---LC---GGLMRVLAQRMME-----RLKTVAGSKMOGLERVNTETIHF-VTK----- 110
DB 161 RLICSTSGGFEPPRLA--WMEDGEELNNAVNTVDDDLTELXSVSSLEDFVNTGNHSTIV 218
OY 111 CAFQPPPSCLRFVQTNISRLQETSEQLVALKWPITRONFSRCLQLQCPDSDSTLPPWS 170
DB 219 C-----LTKYGELSVSQIF-----PWS 235
OY 171 PRPLEATAPAPQPPLLL-LLLPV-GILLILAA--WCL-----HMORTRRRTPRPG 218
DB 236 -KPKQ-----EPIIDLPEFWIITPVSGALVLTAVVLYCLACRHVARMKRRRNEETVG 287
OY 219 -EQVPPV 224
DB 288 TERLSPI 294

RESULT 15
PCT-US02-21694-15
; Sequence 15, Application PC/TUS0221694
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: GPCs AS MODIFIERS OF THE IRRTK AND P21 PATHWAYS AND METHODS OF
; FILE REFERENCE: EX02-081C-PC
; CURRENT APPLICATION NUMBER: PCT/US02/21694
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/305,016
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/328,507
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15


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Query Match      7.0%; Score 87.5; Da 6; Length 239;
Best Local Similarity 21.1%; Pred. No. 8.7;
Matches 40; Conservative 23; Mismatches 78; Indels 49; Gaps 7;

OY 34 HSPSPDSEAFKATIELSDYL-----LDQPVYASMLQDEELCGGLMKRLVLAQ----- 80
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 42 NPLINRDAAVSCLERMKNYLKPSIKKGSITLEEORLRYLVLTQATH--GNMKKIAAYGVGRT 99
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 81 -----RMERLTK-----TVAGSKMGQGLLERYNETIHHVTFCAQFOPPSCL 120
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 100 AKRLGKAMVEYFKKQORETKGNSCTIDPLISDSKYEHL-----SFAERLVKERPSPSF 153
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 121 RFGVQTNISRLQETSQVALKP--MITEQN-----SRLEIQQCPDSITLPPWMSR 172
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 154 VMATSNSSFLHADAPARPALLPSPMLSNSGTAPVPKPPSPSVTUSLSFTVAAPPPWLPQ 213
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 173 PLEATAPATAP 182
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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RESULT 22
US-10-108-605-57
; Sequence 57, Application US/10108605
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 09/7761,142
; PRIOR FILING DATE: 2001-01-16

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PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 479
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-10-108-605-57

Query Match 7.0%; Score 87.5; DB 6; Length 479;
Best Local Similarity 22.9%; Pred. No. 20;
Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

QY 1 MTVALPAPSPPTVLL--LLLSGLSGTQDCSFQSPISDPFAVKIRELSDYLDQYP 57
DB 72 MGLSPGSGPQFOIVROKRIIPAMGVSS-----DHTPAPS-FRI-FNSLSS-----T 117
QY 58 VTVAANIODELCGGLMRLVLAQRMMERLKTAVAGSKMGGLLERVNTIEHFVTKCAFQPP 117
DB 118 CSMESSMDDE-----YMELEFMESQO-----QTALGF-----P 146
QY 118 SCLEFVQTNISRLQETSEQVALKP---WTRONFSRCLEI-OCOPDSTLPPMSPRP 173
DB 147 SGLN-----SLISGQIKQPAKSPAGISMRRPSVRCLMSTESNTSTTPPKPTE- 199
QY 174 LEATAPAA---POPPELLLLPLVGLLLAAWCLHMORTRRPRPGEQVPPVPSQDL 230
DB 200 --TARDCFRPRPP-----ASANCSPIQSKRRHRCATVEKENCPAPSPLSQ 242
QY 231 LAYEH 235
DB 243 VTISH 247

RESULT 23
PCT-US02-17598-104
Sequence 104, Application PC/TUS0217598
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, David C.
APPLICANT: Skeiky, Yashir A.W.
APPLICANT: Bhalla, Ajay
APPLICANT: Coler, Rhea N.
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.42012PC
CURRENT APPLICATION NUMBER: PCT/US02/17598
CURRENT FILING DATE: 2002-06-03
NUMBER OF SEQ ID NOS: 137
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 570
TYPE: PRT
ORGANISM: Leishmania major
PCT-US02-17598-104

Query Match 7.0%; Score 87.5; DB 1; Length 570;
Best Local Similarity 26.7%; Pred. No. 25;
Matches 48; Conservative 26; Mismatches 63; Indels 43; Gaps 10;

QY 4 LAPWSPPTVLLLLLSGLSGTQDCSFQSPISDPFAVKIRELSDYLDQYPVTT--- 59
DB 174 LPPWSSMPNINAVELKRLKLSGT-----LPADWS-SLKSLSNVLEDTPTGILLP 223
QY 60 --VASNIODELCGGLMRLV--LAQRW--MERLK--TVAGSKMGGLLERVNTIEHFVTKC 111

DB 224 PNASLRIQDLVIRKUKLTPLEPPWSSMKITQVLTIDGQVSGTL----- 270
QY 112 AFOPPSCLRFVQTNISRLQETSEQVALKP---WTRONFSRCLEI-OCOPDSTLPPMSPRP 170
DB 271 ---PPWSSAMASVRLINL--EGTEVSGTLPPEWISMSRL-QTINLRRTKVSGLTLPPEWS 323

RESULT 24
US-10-032-214-174

Sequence 174, Application US/10032214

GENERAL INFORMATION:
APPLICANT: PUNNONEN, JUHA
APPLICANT: LAZETIC, ALEXANDRA
APPLICANT: LEONG, STEVEN R.
APPLICANT: CHANG, CHIA-CHUN
APPLICANT: APT, DORIS
APPLICANT: GUSTAFSSON, CLAES
TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
FILE REFERENCE: 02-106730US
CURRENT APPLICATION NUMBER: US/10/032,214
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 09/888,324
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: PCT/US01/19973
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/241,245
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 320
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 174
LENGTH: 303
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (75)
OTHER INFORMATION: Variable amino acid
US-10-032-214-174

Query Match 7.0%; Score 87; DB 6; Length 303;
Best Local Similarity 24.0%; Pred. No. 13; Mismatches 66; Indels 82; Gaps 18;
Matches 58; Conservative 36;

QY 15 LLLLSGLSGTQDCSFQSPISDPFAVKIRELSDYLDQ---DYPTVASNLQDEE--- 68
DB 103 IVIALLRISDSGTYCTVQKPKDKG--AVKLEHLTSVRLMIRADPPPTINDLNPSPNI 160
QY 69 ---LC---GGINRLVLAQRMMERLKTAVAGSKMGGLLERVN---TEHFFVTKCAFQPPPS 118
DB 161 RRLICSTSGGPRPHL--YMLEN-----GPELNATNTVSDQPGELTMIS-----S 205
QY 119 CLRFVQTNISRLQETSEQVALKP---WTRONFSRCLEI-OCOPDSTLPPMSPRP 175
DB 206 ELDFNVN-----NHSIVCLIKYGELLVSGIF-----PMS-KPKQ 239
QY 176 ATAPAPQPPPLLI---LLLPV-GLLLAA--WCL-----HMORTRRRPRPG-ECVP 222
DB 240 -----EPPIQILPFVWIIIPVSGALVLAVALVYCLACHRAVAMRRTRRNEETVGTERTLS 292
QY 223 PV 224
DB 293 PI 294

RESULT 25
US-10-032-214-177

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; Sequence 177, Application US/10032214
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; APPLICANT: LAZETIC, ALEXANDRA
; APPLICANT: LEONG, STEVEN R.
; APPLICANT: CHANG, CHIA-CHUN
; APPLICANT: APT, DORIS
; APPLICANT: GUSTAFSSON, CLAES
; TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
; FILE REFERENCE: 02-10673005
; CURRENT APPLICATION NUMBER: US/10/032,214
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 09//888,324
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19973
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,946
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/241,245
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 177
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-032-214-177
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Query Match 7.0%; Score 87; DB 6; Length 303;
Best Local Similarity 24.4%; Pred. No. 13;
Matches 59; Conservative 34; Mismatches 67; Indels 82; Gaps 18;

QY 15 LLLLLSSGLSTGQDSCFQHSPISSDFAVKIRELSOYLQ---DYPVTVASNLQDEE--- 68
Db 103 IYILALRLSDSGTYTCYVQKRVKLG--AYKLEHLASVRLMIRADFPVPTINDLGNPSPNI 160
QY 69 ---LC--GGLWRLVLAQRMERLKTVAGSKMOGLLERN---TEIHFTKCAFQPPPS 118
Db 161 RRLICSTSGGFP RPRL--YWLEN---GSELNATNTVTSODPGTELYMIS-----S 205
QY 119 CLRFVQTNISRLQETSEDLVAKPW---ITRQNFSCLELQCPDSDSTLPPMSRPPL 175
Db 206 ELDPNVTN-----NHSIVCLIKIGELSVSOLF-----PWS-KPKQ 239
QY 176 ATAPTAPQP--LLLLLLPV-GLLLAA--WCL-----HMQTRRRRTPRG-EQVP 222
Db 240 -----EPPIQLPFLVITIPVSGALVLTAVVLYCLACRHVARWKRTRRNETVGTERTLS 292
QY 223 PV 224
Db 293 PT 294
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Search completed: August 6, 2002, 09:41:14
Job time: 225 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:34:49 ; Search time 22.73 Seconds

(Without alignments)
252,530 Million cell updates/sec

Title: US-09-448-378-1

Perfect score: 1242

Sequence: 1 MVLAPAWSPPTLYLLLL.....RPGQVPPVSPQDLLEH 235

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 US-08-243-545-6	Sequence 6, Appl1
2	1242	100.0	235	2 US-08-993-962-6	Sequence 6, Appl1
3	1242	100.0	235	4 US-09-160-841-6	Sequence 6, Appl1
4	1242	100.0	235	4 US-09-109-100-1	Sequence 1, Appl1
5	1242	100.0	235	5 PCT-US94-05365-6	Sequence 6, Appl1
6	1124	90.5	212	4 US-09-109-100-10	Sequence 10, Appl1
7	1114	89.7	209	4 US-09-109-100-18	Sequence 18, Appl1
8	1110	88.4	209	4 US-09-109-100-9	Sequence 9, Appl1
9	1110	88.4	209	4 US-09-109-100-12	Sequence 12, Appl1
10	1110	88.4	209	4 US-09-109-100-14	Sequence 14, Appl1
11	1110	88.4	209	4 US-09-109-100-17	Sequence 17, Appl1
12	1108	89.2	209	4 US-09-109-100-11	Sequence 11, Appl1
13	1108	89.2	209	4 US-09-109-100-15	Sequence 15, Appl1
14	1107	89.1	209	4 US-09-109-100-13	Sequence 13, Appl1
15	1106	88.0	209	4 US-09-109-100-8	Sequence 8, Appl1
16	1100	88.6	209	4 US-09-109-100-16	Sequence 16, Appl1
17	768.5	61.9	231	1 US-08-243-545-2	Sequence 2, Appl1
18	768.5	61.9	231	2 US-08-993-962-2	Sequence 2, Appl1
19	768.5	61.9	231	4 US-09-160-841-2	Sequence 2, Appl1
20	768.5	61.9	231	5 PCT-US94-05365-2	Sequence 2, Appl1
21	765.5	61.6	231	1 US-08-220-379B-7	Sequence 7, Appl1
22	765.5	61.6	231	5 PCT-US95-03866-6	Sequence 6, Appl1
23	506.5	40.8	137	4 US-09-109-100-19	Sequence 19, Appl1
24	154	12.4	42	5 PCT-US94-05150-17	Sequence 17, Appl1
25	91.5	7.4	675	1 US-08-317-522A-9	Sequence 9, Appl1
26	91.5	7.4	675	1 US-08-439-818A-9	Sequence 9, Appl1
27	91.5	7.4	675	2 US-08-751-965-9	Sequence 9, Appl1

28	91.5	7.4	675	2 US-08-738-975-9	Sequence 9, Appl1
29	91.5	7.4	675	2 US-08-728-626-9	Sequence 9, Appl1
30	91.5	7.4	675	3 US-08-808-599A-9	Sequence 9, Appl1
31	87.5	7.0	415	4 US-09-006-353A-6	Sequence 6, Appl1
32	85	6.8	366	1 US-08-004-492-8	Sequence 8, Appl1
33	84.5	6.8	913	1 US-08-445-640-4	Sequence 4, Appl1
34	84.5	6.8	913	3 US-08-170-558-4	Sequence 4, Appl1
35	84.5	6.8	913	3 US-08-147-314-4	Sequence 4, Appl1
36	84.5	6.8	913	3 US-08-445-461-4	Sequence 4, Appl1
37	84	6.8	107	4 US-09-220-528-52	Sequence 52, Appl1
38	84	6.8	220	4 US-09-220-528-26	Sequence 26, Appl1
39	83.5	6.7	429	1 US-07-964-589-2	Sequence 2, Appl1
40	83.5	6.7	429	5 PCT-US93-02024-2	Sequence 2, Appl1
41	83.5	6.7	671	3 US-09-121-321-16	Sequence 16, Appl1
42	83.5	6.7	671	4 US-08-933-803A-16	Sequence 16, Appl1
43	83	6.7	726	5 PCT-US94-05150-12	Sequence 12, Appl1
44	83	6.7	726	1 US-07-756-250-16	Sequence 16, Appl1
45	82.5	6.6	249	2 US-08-632-514C-11	Sequence 11, Appl1
46	82.5	6.6	249	3 US-09-188-177-11	Sequence 11, Appl1
47	82.5	6.6	513	2 US-08-357-533A-11	Sequence 11, Appl1
48	82.5	6.6	513	2 US-08-459-009-11	Sequence 11, Appl1
49	82.5	6.6	513	3 US-08-459-951-11	Sequence 11, Appl1
50	82.5	6.6	528	4 US-08-928-213B-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-243-545-6
; Sequence 6, Application US/08243545
; Patent No. 5554512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for fli3/fliK-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/243,545
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.6e-117; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
DB 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
QY 61 ASNLODEELCGIMRLVLAQRMMERLKTVAAGSKMOGLLERVNTLHFVTKCAFQPPSCL 120
DB 61 ASNLODEELCGIMRLVLAQRMMERLKTVAAGSKMOGLLERVNTLHFVTKCAFQPPSCL 120
QY 121 RFOVNTNLSRLQETSEQLVAKPMTTRONFSRCLLELOCOPDSSTLPPMSRPLEATAPT 180
DB 121 RFOVNTNLSRLQETSEQLVAKPMTTRONFSRCLLELOCOPDSSTLPPMSRPLEATAPT 180
QY 181 APOPLLILLLLPVGILLAAACLMWORTRRTRPRGEOVPPVPSPDILLVEH 235
DB 181 APOPLLILLLLPVGILLAAACLMWORTRRTRPRGEOVPPVPSPDILLVEH 235

RESULT 2
US-08-993-962-6
Sequence 6, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.6e-117; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
DB 1 MTVLAPAMSPPTTYLLILLSSGLSGTODCSFQHSPISSDPAVKIRELSDYLLQDYPTV 60
QY 61 ASNLODEELCGIMRLVLAQRMMERLKTVAAGSKMOGLLERVNTLHFVTKCAFQPPSCL 120
DB 61 ASNLODEELCGIMRLVLAQRMMERLKTVAAGSKMOGLLERVNTLHFVTKCAFQPPSCL 120
QY 121 RFOVNTNLSRLQETSEQLVAKPMTTRONFSRCLLELOCOPDSSTLPPMSRPLEATAPT 180
DB 121 RFOVNTNLSRLQETSEQLVAKPMTTRONFSRCLLELOCOPDSSTLPPMSRPLEATAPT 180
QY 181 APOPLLILLLLPVGILLAAACLMWORTRRTRPRGEOVPPVPSPDILLVEH 235
DB 181 APOPLLILLLLPVGILLAAACLMWORTRRTRPRGEOVPPVPSPDILLVEH 235

RESULT 3
US-09-160-841-6
Sequence 6, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:


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QY 1 MTVLAPAMSPPTTYLLLLLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYPVY 60
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 1 MTVLAPAMSPPTTYLLLLLLLLSSGLSTGDCSFQHSPISSDFAVKIRELSDYLLQDYPVY 60
QY 61 ASNIODEELCGGIMRLVLAQRMERIKTVAGSKMOGLLEVRNTEIHFTVKCAFQPPPSCL 120
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 61 ASNIODEELCGGIMRLVLAQRMERIKTVAGSKMOGLLEVRNTEIHFTVKCAFQPPPSCL 120
QY 121 RFQVQNISRLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 121 RFQVQNISRLQETSEQLVALKPWITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPT 180
QY 181 APOPRLILLLLPVGLLLAAAWCLHMORTRRTPRPGEQVPPVSPQDILLVEH 235
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 181 APOPRLILLLLPVGLLLAAAWCLHMORTRRTPRPGEQVPPVSPQDILLVEH 235

RESULT 6
US-09-109-100-10
; Sequence 10, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 10
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-10

Query Match 90.5%; Score 1124; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.1e-105;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SGQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGIMRLVLAQRMER 84
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 2 SGQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGIMRLVLAQRMER 61
QY 85 RLKTVAGSKMOGLLEVRNTEIHFTVKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPM 144
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 62 RLKTVAGSKMOGLLEVRNTEIHFTVKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPM 121
QY 145 ITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPTAPQPPILLLLPVGLLLAAAWC 204
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 122 ITRQNSRCLELQCPDSSSTLPPWSPRPLEATAPTAPQPPILLLLPVGLLLAAAWC 181
QY 205 LHMORTRRTPRPGEQVPPVSPQDILLVEH 235
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 182 LHMORTRRTPRPGEQVPPVSPQDILLVEH 212

RESULT 7
US-09-109-100-18
; Sequence 18, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 18
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; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-18

Query Match 89.7%; Score 1114; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e-104;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGIMRLVLAQRMERL 86
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNIODEELCGGIMRLVLAQRMERL 60
QY 87 KTVAGSKMOGLLEVRNTEIHFTVKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPMIT 146
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 61 KTVAGSKMOGLLEVRNTEIHFTVKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPMIT 120
QY 147 RQNSRCLELQCPDSSSTLPPWSPRPLEATAPTAPQPPILLLLPVGLLLAAAWCLH 206
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 121 RQNSRCLELQCPDSSSTLPPWSPRPLEATAPTAPQPPILLLLPVGLLLAAAWCLH 180
QY 207 WQTRRRTPRPGEQVPPVSPQDILLVEH 235
; TYPE: PRT
; ORGANISM: Homo sapiens
Db 181 WQTRRRTPRPGEQVPPVSPQDILLVEH 209

RESULT 9
US-09-109-100-12
; Sequence 12, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
```



```
QY      87 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
QY      207 WQTRRRTRPRGEOVPVPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEOVPVPVPSPODLLVEH 209
```

```
RESULT 13
US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15
```

```
Query Match      89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.3e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 86
      |||||||
Db      1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 60
QY      87 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
QY      207 WQTRRRTRPRGEOVPVPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEOVPVPVPSPODLLVEH 209
```

```
RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13
```

```
Query Match      89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 5.4e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 86
      |||||||
Db      1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 60
QY      87 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
QY      207 WQTRRRTRPRGEOVPVPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEOVPVPVPSPODLLVEH 209
```

```
RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8
```

```
Query Match      89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      27 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 86
      |||||||
Db      1 TODCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEELCGLMRLVLAQRMERL 60
QY      87 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 146
      |||||||
Db      61 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPPSCLRFVQTNISRLLOETSEOLVALKPWIT 120
QY      147 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 206
      |||||||
Db      121 RQNFSCLELQOCOPDSSSTLPPWSPRPLEATAPAPQPLLILLIPVGLLLAAACMLH 180
QY      207 WQTRRRTRPRGEOVPVPVPSPODLLVEH 235
      |||||||
Db      181 WQTRRRTRPRGEOVPVPVPSPODLLVEH 209
```

```
RESULT 16
US-09-109-100-16
; Sequence 16, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
```

;; CURRENT FILING DATE: 1998-07-02
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 16
;; LENGTH: 209
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-109-100-16

Query Match 88.6%; Score 1100; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 2, 7e-103;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDGFHSPISDFPAVKIRELSYLLQDYPVYVSNLQDEELCGGIMRLVLAQRMERL 86
DB 1 TQDGFHSPISDFPAVKIRELSYLLQDYPVYVSNLQDEELCGGIMRLVLAQRMERL 60
QY 87 KTVAGSKMGLLEEVNTEIHFVTKCAFPQPPSCLEFVQTNISRLQETSQYVALKPWIT 146
DB 61 KTVAGSKMGLLEEVNTEIHFVTKCAFPQPPSCLEFVQTNISRLQETSQYVALKPWIT 120
QY 147 RQNSRCLFQCPDSSSTLPPWSPRELEATAPAPQPLLLLPVGLLLAAACMLH 206
DB 121 RQNSRCLFQCPDSSSTLPPWSPRELEATAPAPQPLLLLPVGLLLAAACMLH 180
QY 207 WQTRRRTPRRGEVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRRGEVPPVPSPODLLVEH 209

RESULT 17
US-08-243-545-2
; Sequence 2, Application US/08243545
; Patent No. 5554512

;; GENERAL INFORMATION:
;; APPLICANT: Lyman, Stewart D.
;; APPLICANT: Beckmann, M. Patricia
;; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.0.1
;; SOFTWARE: Microsoft Word, Version #5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/243,545
;; FILING DATE: 11-MAY-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/162,407
;; FILING DATE: 03-DEC-1993
;; APPLICATION NUMBER: 08/111,758
;; FILING DATE: August 25, 1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/106,463
;; FILING DATE: August 12, 1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/068,394
;; FILING DATE: May 24, 1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Malaska, Stephen L.
;; REGISTRATION NUMBER: 32,655

;; REFERENCE/DOCKET NUMBER: 2813-C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 587-0430
;; TELEFAX: (206) 233-0644
;; TELEEX: 756822
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 231 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-243-545-2

Query Match 61.9%; Score 768.5; DB 1; Length 231;
Best Local Similarity 70.3%; Pred. No. 8e-70;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MVLAPAWSP-TTYLLILLSSGSGTQDCSFQHSPISSDFPAVKIRELSYLLQDYPT 59
DB 1 MVLAPAWSPNSLLILLLLSPCLRGTPDCYFSSHSPISSNFKVFRRLTDHLKDYPT 60
QY 60 VASNLQDEELCGGIMRLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAFPQPPSC 119
DB 61 VAVNLQDEELCGGIMRLVLAQRMERLKTAVGSKMGLLEEVNTEIHFVTKCAFPQPPSC 120
QY 120 LRFVQTNISRLQETSQYVALKPWITR--QNSRCLFQCPDSSSTLPPWSPRELEAT 177
DB 121 LRFVQTNISRLQETSQYVALKPWITR--QNSRCLFQCPDSSSTLPPWSPRELEAT 180
QY 178 APTAPQP--LLILLLPVGLLLAAACMLHQRTRRRTPRRGEVPPVPSP 227
DB 181 ELPEPRQQLLLILLLPVGLLLAAACMLHQRTRRRTPRRGEVPPVPSP 228

RESULT 18
US-08-993-962-2
; Sequence 2, Application US/08993962
; Patent No. 5843423

;; GENERAL INFORMATION:
;; APPLICANT: Lyman, Stewart D.
;; APPLICANT: Beckmann, M. Patricia
;; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98101
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 7.0.1
;; SOFTWARE: Microsoft Word, Version #5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/993,962
;; FILING DATE: December 18, 1997
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/162,407
;; FILING DATE: December 3, 1993
;; APPLICATION NUMBER: 08/111,758
;; FILING DATE: August 25, 1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/106,463
;; FILING DATE: August 12, 1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/068,394
;; FILING DATE: May 24, 1993

RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 231
US-08-220-379B-7

Matches 162; Conservative 18; Mismatches 43; Indels 9; Gaps 4;

OPERATING SYSTEM: PC-DOS/MS-DOS

GENERAL INFORMATION: Michiko N.
APPLICANT: Fukuda, N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
TITLE OF INVENTION: Trophinin
NUMBER OF INVENTION: Proteins
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/317,522A
APPLICATION NUMBER: US/08/317,522A
FILING DATE: 04-OCT-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 675 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-317-522A-9

Query Match	7.48;	Score 91.5;	DB 1;	Length 675;
Best Local Similarity	27.7%;	Pred. No. 0.57;		
Matches	31;	Conservative	13;	Mismatches 29;
				Indels 39;
				Gaps 4

```

0Y      111  CAAPPCSCAEVQTINISRLQETSEEDVLLKPKITQONSRCLECCQDPSSTLPWMS 170
      1:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      2  CSRDPHSC-----VPLLSKRLSRAPLPRKGPSINHQLVYNN-----KPFSS 46

0Y      171  PRPEATAPAPOPPLLILLIPYGLILLAAACMLQWRTRRRTPRGEQVP 222
      47  PTP-----PTTRKPLPLPKLL-----RKTPDSSPTVP 74

```

```
Search completed: August 6, 2002, 09:39:37
Job time: 288 sec
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:40:23 ; Search time 32.24 Seconds

(without alignments)
688.481 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MTVLAPAMNSPLLILL.....MORARRGELHPGVLPDPSHP 231

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1223	100.0	231	2	A49265	flt3/flk-2 ligand
2	879	71.9	220	2	S43291	FLT3/FLK2 ligand (
3	879	71.9	220	2	I58343	flt3 ligand isofor
4	768.5	62.8	235	2	I38440	flt3 ligand - huma
5	616.5	50.4	245	2	S43293	FLT3/FLK2 ligand (
6	594.5	48.6	178	2	I39076	flt3 ligand altern
7	95.5	7.8	909	1	A54809	disease resistance
8	88	7.2	843	2	T01438	hypothetical prote
9	87	7.1	291	2	AF0123	probable antigenic
10	86	7.0	962	2	C71617	SERA antigen/papal
11	85	7.0	181	2	T20323	hypothetical prote
12	84.5	6.9	939	2	E82121	peptidase, insulin
13	84	6.9	1409	2	T37188	presynaptic activi
14	83.5	6.8	552	1	A31401	macrophage colony
15	83.5	6.8	552	1	S35703	colony-stimulating
16	83.5	6.8	2476	2	T344022	zonahesin - pig
17	82.5	6.7	378	2	S00842	leukostatin precur
18	82.5	6.7	431	2	T04868	hypothetical prote
19	81	6.6	4131	2	T21085	hypothetical prote
20	80.5	6.6	391	2	B40892	apolipoprotein A-I
21	80.5	6.6	394	2	A25281	apolipoprotein A-I
22	80.5	6.6	395	2	A40892	apolipoprotein A-I
23	80	6.5	382	2	E84527	hypothetical prote
24	79.5	6.5	399	2	C40892	apolipoprotein A-I
25	79.5	6.5	745	2	T38299	probable beta-adap
26	79	6.5	1101	2	S58108	hypothetical prote
27	78.5	6.4	122	2	D70730	hypothetical prote
28	78.5	6.4	315	2	T24821	hypothetical prote
29	78.5	6.4	379	2	T11349	ubiquinol--cytochr

30	78.5	6.4	468	2	T23091	hypothetical prote
31	78.5	6.4	3068	1	A44062	genome polyprotein
32	78	6.4	224	2	I37243	CKR-35 antigen
33	78	6.4	743	2	T34632	probable bi-functi
34	78	6.4	806	2	E64221	phenylalanine--trn
35	78	6.4	908	2	S51293	probable membrane
36	78	6.4	1601	2	AE2011	hypothetical prote
37	78	6.4	1715	2	T06145	disease resistance
38	77.5	6.3	266	2	A45844	MHC class II histo
39	77.5	6.3	456	2	B72130	frame-shift with c
40	77.5	6.3	579	2	JC7629	membrane-type friz
41	77.5	6.3	746	2	S67203	probable membrane
42	77.5	6.3	774	2	B86492	hypothetical prote
43	77.5	6.3	774	2	H81540	hypothetical prote
44	77.5	6.3	811	2	E72003	hypothetical prote
45	77	6.3	619	2	D86509	s/T protein kinase
46	77	6.3	619	2	A72114	sodium/phosphate c
47	77	6.3	653	2	A54366	hypothetical prote
48	77	6.3	1509	2	T19486	conserved hypothet
49	76.5	6.3	222	2	D59026	glycoprotein VP7 p
50	76.5	6.3	326	1	VGXR15	

ALIGNMENTS

RESULT 1

A49265
flt3/flk-2 ligand precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C:Accession: A49265; I49347; I49346; S43290

R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Hoall
D.; Williams, D.E.; Beckmann, M.P.
Cell 75, 1157-1167, 1993

A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a

A:Reference number: A49265; MUID:94084791

A:Accession: A49265

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-231 <LYM>

A:Cross-references: GB:I23636; NID:9439441; PIDN:AAA9436.1; PID:9439442

A:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.

A:Reference number: I39075; MUID:96032581

A:Accession: I49347

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-197, 'V', 198-231 <RE2>

A:Cross-references: EMBL:U29875; PID:91072039; PIDN:AAA90951.1; PID:91072040

R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zuzawski, S.; Bazan, J.F.;
felt, A.; Muench, M.; Kelnner, G.; Namiyawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik
Nature 366, 643-648, 1994

A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi

A:Reference number: S43290; MUID:94195428

A:Accession: S43290

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197, 'V', 198-231 <HAN>

A:Experimental source: clone T110

A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-

C:Genetics:

A:Insertions: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3

C:Keywords: transmembrane protein

Query Match 100.0%; Score 1223; DB 2; Length 231;

OY 149 ACQNFSCLEVOQCPDSSTLLPPRSPIALTEATEPEPRROLTLTLPLTVLLAAW 208
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 715 HGRNRR-LSIKSCHDELIV---TPADFENDMLPS--LEVLTHSLHNLTRV-----W 762

OY 209 G 209
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 763 G 763

RESULT 8
 T01438
 hypothetical protein GS034D21.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 05-Nov-1999
 C:Accession: T01438

R:Smith, A.; Harmon, G.; Elliott, G.; Tryman, B.
 Submitted to the EMBL Data Library, November 1997
 A:Description: The sequence of H. sapiens BAC clone GS034D21.
 A:Reference number: Z14332

A:Accession: T01438
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-843 <SMI>
 A:Cross-references: EMBL:AC003077; NID:g2588634; PIDN:AAH83946.1; PID:g2588635
 C:Genetics:
 A:Map position: 7
 A:Note: intron positions not resolved (incomplete sequence)
 A:Note: WUGSC:H_GS034D21.1

Query Match 7.28; Score 88; DB 2; Length 843;
 Best Local Similarity 20.18; Pred. No. 8.7;
 Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

OY 27 GTPPCYFHSHPISNFKFRELTDHLK--DYPVTVAVNLQDEKCKALW----SLFL 79
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 483 GVPD-----NIKSFYK-----NHMKRYDRPFHKGR-DKENEFKSLWERTSLYL 529

OY 80 AQ-----RW-IEQLTVAGSKMOT--LLEDVNTIEH-FVTSQ-----TPQPLPECT 121
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 530 VQSLPGISRWFEVKEKREVENSPLENAIEYLENNQOLKTLISQCCQRQMONINPLMCL 569

OY 122 -----RYV 124
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 590 NGVIDAANGVSNRYOAFVKEYIILSHPEDGKIARLEMLEQAQILEGLAVHEKRV 649

OY 125 QTNISHLKDTCTQLALPKIGKACQNFSCLEVO-----CQ-----PDS 165
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 650 PDMRPLHKTLVDQEFVFKSSLG--IQEFSACMQASVYHPNPGSPVCRNSARASVSPDG 707

OY 166 STLLPPRSPIALFA 179
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 708 TRVIRPRSPISYPA 721

RESULT 9
 AF0123
 probable antigenic leucine-rich repeat protein YP01006 [imported] - Yersinia pestis (str
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AF0123
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 demo-Tarraga, A.M.; Chillingworth, T.; Croxin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AF0123
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-291 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC89849.1; PID:g15979075; GSPDB:GN00175
 C:Genetics:

A:Gene: YP01006

Query Match 7.1%; Score 87; DB 2; Length 291;
 Best Local Similarity 23.8%; Pred. No. 3.2;
 Matches 50; Conservative 30; Mismatches 62; Indels 68; Gaps 11;

OY 56 DYPVTVAVNLQDEKCKALMSFLAQRWIEQLKYVAG-----SKMOTLEDVNTIEHF 108
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 24 DRPAATALTLPAD---YHAIW-----EKWENDRPTVAGRGQAVARMECLEN-NAERLN 74

OY 109 VNSCTFQPLPE---C--LRFVQTNISHL-----LKDTCTQLALPKIGKACQ 152
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 75 LSSLDITSLPDLPCNENLITCNITELPTLPNLOTKASVQNLKTPVTPASLIS 134

OY 153 FS-----RCLEVOQCPDSSTLLPPRSPIALFA-----TELP----- 183
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 135 LKVNHELERLPEPLPEGLKTLVDGC--NTSLQPSRLPPVLESLSISNCLTELPPLN 192

OY 184 -----EPRROLTLTLPLTVLLAAW 208
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 193 SLKELDAGNQLRLPDTLPISLRINAV 222

RESULT 10
 C71617
 SERA antigen/papain-like proteinase with active Ser PFB0345C - malaria parasite (Plas
 C:Species: Plasmodium falciparum
 C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
 C:Accession: C71617

R:Gardner, M.J.; Tetteh, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
 ; Perera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
 Science 282, 1126-1137, 1998
 A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A:Reference number: A71600; MUID:99021743

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-962 <GAR>
 A:Cross-references: GB:AE001388; GB:AE001362; NID:g3845157; PIDN:AAC71858.1; PID:g384
 A:Experimental source: clone 3D7
 C:Genetics:
 A:Gene: PFB0345C
 A:Superfamily: Plasmodium vivax serine-repeat antigen

Query Match 7.0%; Score 86; DB 2; Length 962;
 Best Local Similarity 20.9%; Pred. No. 15;
 Matches 31; Conservative 28; Mismatches 39; Indels 50; Gaps 7;

OY 8 WSPNSLLLLLLSPCLRGTPDCYFHSHPISNF-----KYKRELTDHL----- 53
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 422 WMKNTGELL-----PQLSYDLTYKNNFTERTONKSTSQNIYDKLCHNHEYC 470

OY 54 --LKDYPTVA-VNLQDEKCKALMSFLAQRWIEQLKYVAGSKMOTLEDVNTIEHF 110
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 471 NKLKHNKNCISKINVEDKNCALSWA-FASKYHLETTIKMKG-----YELINASVLYVT 523

OY 111 SCTFQPLPECFVQTNISHLKDTCTQ 138
 :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
 Db 524 NC-----LKNKMKDYCTE 536

RESULT 11
 T20323

hypothetical protein D1086.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20323
 R:Smey, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19257

A:Accession: T20323

A:Status: preliminary; translated from GH/EMBL/DDDB
A:Molecule type: DNA
A:Residues: 1181 <MIL>
A:Cross-references: EMBL:Z81491; FIDN:CA804019.1; GSPDB:6N00023; CESP:DI086.1
A:Experimental source: clone DI086
C:Genetics:
A:Gene: CESP:DI086.1
A:Map position: 5
A:Introns: 112/3; 132/3; 167/3

Query Match	7.0%	Score 85	DB 2	Length 181
Best Local Similarity	23.5%	Pred. No. 2.8		
Matches 39; Conservative	24	Mismatches	59	Indels 44
				Gaps 8

```
QY      13 SLLELLLLLPCLRGTPDCYFESHSPISSENFVKVRFELTDLKLD-----YPTVAANLQD 67
      ::  || ||  ||  ::  :  : || ||  :  :  :  :
Db      8 TILPFLFLSKAENSLPDCSKDQLQITWTCRPKIAKLTDMKKNPNINSGFPSVETLN-KM 66
```

```

0Y      68 EKHCALMSLELAQRNTEQLKTVAGSKMOTLLEDVNTETHFVTSCTFQPLP----- 118
      :||      | : : : : : : : : : :
Db      67 SGYCT-----EAMSCVSPAKPAITERKSKFATMCTIDFNSGPGYACAA 111

```

```
QY      119 -----ECLRFVQTINISHLKD-TCQLLAKPCI----GKAC   150  
          ||::: ::| : | | | | | | | |  
Db      112 KLKASNDKTECVOWYFSDKSRLMSTDOKCAOFKAKKOIEKDFGAK  157
```

RESULT 12

peptidase, insulinase family VC2072 [imported] - Vibrio cholerae (strain N16961 serogroup C:Species: Vibrio cholerae
C.Date: 18-Aug-2000 #sequence revision 20-Aug-2000 #text change 02-Feb-2001

R. Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Frischholz, L.G.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoli, I.; Sellers, J.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Accession: E82121
 A:Reference number: A82035; MUID:20406833
 Attribute: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*
 Feature: 400, 417-403, 2000
 Feature: 400, 417-403, 2000

A: scacusi: preterminaly
A: Molecule type: DNA
A: Residues: 1-939 <HEI>
A: Cross-references: GR: AF004281. GR: AF003852. NIT: 066566616;
RTDN: 0665319. 1. GENDP: GND01

A:Experimental source: serogroup O1; strain N16961; biotype El Tor
A:Gene: VC2072
A:Map position: 1

```
c/superfamily: insulin
```

Model	Best Local Similarity	Pred. No. 20;	Mismatches	Indels	Gaps
Conservative	24.6%;	20;	30;	72;	85;
Matches	61;				15;

Db 587 SGEISQKLPOLMEVILKKFAQRDFQPKRPATIKQOMTRNNRNNAAHDKPISQLENAMTGLD 646

```

Db 647 PNPFPYAEIIAIDVQVEELAHFVDITLSQLHVEFMFYGDWPAEAAHK-----MAEVLK 701
      ::  ::  |  ||  :  |  |  :  ::  ::  |

```

Db 702 DALRYGGTTESLRLVLMGKS-GTQR--EVQCCQDDSAIVVYYQSHEVSPRS-ITALY 757

```

      || | | : | : : : ||
Db  758 SLANILMSATFFHEITKQQLGVMVGIMPL-----NRHGLIL 797

```

Db 798 YVQSPSAP 805

RESULT	13
T37188	

C:Accession: T37188
 C:Species: *Caenorhabditis elegans*
 C:date: 03-Dec-1999 #sequence_revision: 03-Dec-1999 #text_change: 18-Feb-2000

A: Description: The sequence of *C. elegans* cosmid C02H7
A: Reference number: Z20523
submitted to the EMBL Data Library, February 1996
R. Belmadani, D. J. Minn, M.

A/Accession: 13/100
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1409<|ET>

A:Gene: *aez-3*; CESP.C02H7.3
A/Cross-References: EMBL:U099945; PIDN:AC047920.1; GSPDR:GN000025
A/Experimental source: strain Bristol N2; clone C02H7
C/Genetics:

A:map position: X
A:introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 689/3; 782/2

Query Match	6.9%;	Score 84;	DB 2;	Length 1409;
Best Local Similarity	23.9%;	Pred. No. 36;		
Matches 54:	Conservative 31;	Mismatches 73;	Indels	

QY 4 LAPANSPNSLLLLLLSPLCIGTPTDCFTFSHPISSNFKVKFREL-TDHLKLDYPVTYA 62
| | : : : | | : : : | | : : : | | : : :
Db 317 LIPAWPDSAE--OILLADMPDTGVDSSEPHNR-----KLRFPSDVITVMDL-THG 366

[illegible]

09	106	-----IHFVTC-----TFQPLECLRFVQTNISHLKDYQTQLALK 143
		: : : : :
Dh	A17	DSIVUACBIVAGUENENANINUCNECEUBABT BY VABDITOT OMBCEI DEBPOCTOT TM D 478

```
QY      144 PCIGACONFSRCLEVQC-PDSSTLPPRSPLATELTELEPRPR 188  
        | : | : | : | : | : | : | :  
DB      476 TCDMAUTENAEQ-000000000000000000000000000000 E1F
```

RESULT 14

macrophage colony-stimulating factor precursor - mouse
N/Alternate names: colony-stimulating factor 1; M-CSF
C(species): Mus musculus (house mouse)

C:Accession: A21401; JN0294; A25575; A23166; A25883
R:Reader, M.B.: Martin, G.A.; Noble, J.A.; Wittman, V.P.; Warren, M.K.; McGrogan, M.;
Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988

A;Reference number: A31401; MUID:88320507
A;Accession: A31401
A;Molecule type: mRNA

A:Cross-references: GB:M21952; GB:U03863; NID:g132804; PIDN:AAA37481.1; PID:3309199
R:Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Broxmeyer,
Gene 102, 165-170, 1991

A:Reference number: JN0294; MUID:91340149
A:Accession: JN0294
A:Molecule type: DNA

A: Cross-references: GB:M81316; GB:M61708; NID:q192802; PILDN:AA1966.1; PID:q192803
R: Delamarier, J.F.; Hession, C.; Simon, D.; Gough, N.M.; Rothenbuhler, R.; Mermod, J.
Nucleic Acids Res. 15, 2389-2390, 1987


```

Db      59 ARASSIP-----CTPLSSFFTSAGASGNTFPP--ELTTSQSEVSTASLVLP 106
QY      51 --DHLKDYPTVAVNLODEKHKALMSLFLAQRWIEOLKTVAGSKMOTLEDVNTIEHF 108
Db      107 KSSGASDPPVIT-----NPATSSAVASTLEFEKGSAPPV-----145
QY      109 VNSCFEQLPECLRVQTNIS-----HLKDYCTQLLAKPCIG 147
Db      146 VTSSTMTSGP---FVATVTSSTSGPPVMTAGSLGPKSETHGLSATIATSSGESSVA 201
QY      148 KACQNFSCRLVOCQDPSSTLLPPRSPIALPATELPEPRPOLLLLLPLTLVLA 207
Db      202 GGTPEVSTKISTSPNNTTTPR-----PGSSGMILVSLIALIVLVLA 249
QY      208 WGLRM-QQARRR 218
Db      250 LLLMROROKRR 261

```

```

RESULT 18
T04868
hypothetical protein F28A21.170 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T04868
R:Bayan, M.; Mueller, M.W.; Mueandlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15387
A:Accession: T04868
A:Molecule type: DNA
A:Residues: 1-431 <BEV>
A:Cross-references: EMBL:AL035526
C:Experimental source: cultivar Columbia, BAC clone F28A21
C:Genetics:
A:Map position: 4
A:Note: F28A21.170

```

```

Query Match
Best Local Similarity 6.7%; Score 82.5; DB 2; Length 431;
Matches 49; Conservative 15; Mismatches 63; Indels 55; Gaps 8;

QY      10 PNSSLLLLLLLS-----PCLRGTPDCYFS---HSPISNFKKRELTHLKNKPY 59
Db      4 PSLPLLLLLLSATISAASLSPTSPTRPKPSSSSSL-----48
QY      60 TVAVNLODEKHKALMSLFL--AQRWIEOLKTVAGSKMOTLEDVNTIEHFVTSCTFOPL 117
Db      49 -----DPRQLKALLESINIPYKDCPNHRPTTKSTSSSVVTCDTSSPRLVMSISF---98
QY      118 PECLRFVQTNISHLKDYCTQLLAKPCIGKACQNFSCRLVOCQDPSSTLLPPRSPIAL 177
Db      99 -----TNCSTDLISITLALRLSPSL--TSLISFLNC-----PSLSP--PPRLPDSL 140
QY      178 EA 179
Db      141 HS 142

RESULT 19
T21085
hypothetical protein F18C12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T21085
R:Haris, B.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19371
A:Accession: T21085
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4131 <WII>

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A:Cross-references: EMBL:Z75536; PIDN:CAA99830.1; GSPDB:GN00019; CESP:F18C12.1
A:Experimental source: clone F18C12
C:Genetics:
A:Gene: CESP:F18C12.1
A:Map position: 1
A:Introns: 54/3; 112/3; 146/1; 294/1; 381/3; 455/3; 596/3; 716/3; 743/2; 782/3; 820/3
09/3; 2303/3; 2483/1; 2529/1; 2612/3; 2687/1; 2734/3; 2799/3; 2841/3; 2891/2; 2932/3;
C:Superfamily: dynein heavy chain, cytosolic

Query Match
Best Local Similarity 6.6%; Score 81; DB 2; Length 4131;
Matches 51; Conservative 28; Mismatches 68; Indels 92; Gaps 11;

QY      47 RELDHLKDYPTVAVNLODE-----KHKALMSLFLAQRWIEOLKTVAGSKMOTLL 99
Db      381 QEYIGHSKSVPSV-----DEPYLGLPEINIKYSQIYADRTTSSITLALGDTKNAL 3864
QY      100 EDVNTIEHFVTS-----CTFOPLPE-----CLRFVQ-----NI 128
Db      3865 SDQSDKISQIVSLMKKLCQSDPLKRELPTAIRSADPISGVLCLETINMLSLIKQLHRSI 3924
QY      129 SHLKDYCTQLLAKPCIGKACQNFSCRLVOCQD-----164
Db      3925 GHVAKSKKTPSLA-SPAVQKTIQS---LVFOQTPEWDSMMAGSPADYLVVYVKTR 3979
QY      165 -----SSTLLPPRSPIALATELPEPR-----PROLLLLLLPLTLVLA 208
Db      3980 GTQLPRESSKSSSL--SSPI--DFSDLYPNIFLNALQTTSRQIKIPLDOLLSSAM 4034

```

```

RESULT 20
B40892
apolipoprotein A-IV precursor - mouse (strain 129)
C:Species: Mus musculus (house mouse)
C:Date: 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 13-Aug-1999
C:Accession: B40892
R:Reue, K.; Leete, T.H.
J. Biol. Chem. 266, 12715-12721, 1991
A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion
A:Reference number: A40892; MUID:91286509
A:Accession: B40892
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-391 <REU>
A:Cross-references: GB:M64248; NID:g191884; PIDN:AAA37214.1; PID:g191885
A:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 2
C:Superfamily: apolipoprotein A-I
C:Keywords: lipid binding, lipoprotein

```

```

Query Match
Best Local Similarity 6.6%; Score 80.5; DB 2; Length 391;
Matches 37; Conservative 42; Mismatches 69; Indels 27; Gaps 6;

QY      11 NSSLLLLLLSPCLR-----GTPDCYFSHPISNFKYK---RELDHL--LK 55
Db      147 NTQTQEMKQLTPYIQRMQTTIKENVNMLHTSMPLATNLKDKFNRMNEELKGLTPRAN 206
QY      56 DYPVTVAVNLODEKHKALMSLFLAQRWIEOLKTVAGSKMOTLEDVNTIEHFVTSCTFO 115
Db      207 ELKATITDNDLELRSLAPLTVGVQEKLNHQWEGIA-FQMKNAEELQTKV-----SAKID 261
QY      116 PLPECLRFVQTNISHLKDYCTQLLAKPCIGKACQNFSCRLVOCQDPSSTLLP 170
Db      262 QL-----QKNLADLVEDVQSKVGNTEGLQKSLHEDLNRLQLEQVEEFRTVPE 309

```

```

RESULT 21
A25281
apolipoprotein A-IV precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 13-Aug-1999

```

C:Accession: A25281
R:Williams, S.C.; Bruckheimer, S.M.; Lusis, A.J.; LeBeauf, R.C.; Kinniburgh, A.J.
Mol. Cell. Biol. 6, 3807-3814, 1986
A:Title: Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by a high-lipid diet
A:Reference number: A25281; MUID:87089722
A:Accession: A25281
A:Molecule type: DNA
A:Residues: 1-394 <MUL>
A:Cross-references: GB:M13966; NID:g192006; PIDN:AAA37253.1; PID:g387102
C:Genetics:
A:Introns: 16/1; 58/2
C:Superfamily: apolipoprotein A-I
Keywords: chylomicron; HDL; lipid binding; lipoprotein

	Query Match	6.6%	Score 80.5;	DB 2;	Length 394;	
	Best Local Similarity	21.9%	Pred. No. 17;			
	Matches 39;	Conservative 41;	Mismatches 65;	Indels 33;	Gaps 77;	
QY	11 NSSLLLLLLSPCLR-----GTPDGYSHSPISSNFKVF---RELTDHL-----53					
DQ	146 NTQGEKQLGLPYIQRMQTIKENVNDLHTSMPLATNLKDKFRNMELKGHLPRAN 205					
QY	54 -LKDYPTAVNLODERHCKALMSLELAQRWTEIDKYAGSKMOTLEDVNTLHEHYTSC 112					
DQ	206 RLK---ATIQNEDEDRSLAPLVGOVEKLHNHGEGLA-FQMKRNMBEELYTKV---SA 257					
QY	113 TFGPRLPCFLAFVQNTINSHLKDPCFQTLAKRCICACAKONSFCELEVOCOPDDSTILP 170					
DQ	258 KIDL-----QKNLPIVEDIQSVKNGKNEGLOKALEDINKALBEQVEEFRTIYEP 308					

RES001 22
 A:0892
 apolipoprotein A-IV precursor - mouse (strain C57BL/6)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 13-Aug-1999
 C:Accession: A40892
 R:Reue, K.; Leete, T. H.
 J. Biol. Chem. 266, 12715-12721, 1991
 A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in
 A:Reference number: A40892; MUID:91286309
 A:Accession: A40892
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-395 <REU>
 A:Cross-references: GB:M4249; NID:G19186; PIDN:AA37215.1; PID:G191887
 A:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207
 C:Superfamily: apolipoprotein A-I
 C:Keywords: lipid binding; lipoprotein

[illegible]

RESULT 23
E84527
hypothetical protein At2g15320 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84527
R:Rill, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C. Y
M.; Koo, H.; Moffett, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon
euss, D.; Niernann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20083487
A:Accession: E84527
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-82 <STD>
A:Cross-references: GB:AE002093; NID:G4662629; PIDN:AMD26901.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g15320
A:Map position: 2

Query Match	6.5%	Score 80	DB 2	Length 382
Best Local Similarity	24.7%	Pred. NO. 18		
Matches 53	Conservative 18	Mismatches 78	Indels 66	Gaps 8
QY	14 LLLLLLSPCGRGPDCCYFSSHPSSINFKVFRRLTHLKDYPYVAVNIQDEKCKA	73		
DB	4 LLLLLL---LFSSADSLTSPDYSA-----LAFATATVPNSIIPMSCLA	47		
QY	74 LMSLFLAQRWIBOLKTVAGSKMOTLLEDVYTHF-----VTSCTFOP-----	116		
DB	48 SMDFTVSDPCASPRRT-----HFCGIGTCSDSSTRTVQLTLDLPAGYNG	90		
QY	117 -----LPECLR--FVQTNISHLKDCQJQLAKPICIGKACQNFSCLEVOQCPDSS	166		
DB	91 RLPPLISGTELTETLDIANNNEVGLIPSSISLTSKTLILNS--NFSQSL-----PDVY	144		

RESULT 24
C40892
apolipoprotein A-IV precursor - mouse
C:Species: Mus musculus castaneus (southeastern Asian house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-1993
C:Accession: C40892
R:Reue, K.; Leete, T.H.
J Biol. Chem. 266, 12715-12721, 1991
A:Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion
A:Reference number: A40892; MUID:91286509
A:Accession: C40892
A:Molecule type: mRNA
A:Residues: 1-399 <REU>
A:Cross-references: GB:M64250
A:Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 2
C:Superfamily: apolipoprotein A-I
C:Keywords: chylomicron; duplication; HDL; lipid binding; lipid transport; lipoprotein

[illegible]

RESULT 25

T38299

probable beta-adaptin clathrin assembly protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03 Dec 1998
 C:Size: 1000
 C:Start: 1000
 C:End: 1000

C/Species: Schizosaccharomyces pombe

```
C:\Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
```

C;Accession: T38299

R; Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21785

A;Accession: T38299

A; Status: preliminary; translated from GB/EMBL/DBJ

A:molecule type: DNA

A;Residues: 1-745 <SKE>

A; Cross-references: EMBL:Z99163; PIDN:CAB16234.1; GSPDB:GN00066; SPDB:SPAC23H3.06

A; Experimental source: strain 972h-; cosmid c23H3

C:Genetics:

A; Gene: SPDB:SPAC23H3.06

A;Map position: 1

A: Introns: 327/3

Query Match

6.58; Score 79.5; DB 2; Length 745;

Best Local Similarity 20.98; Pred. No. 43;

Matches 62; Conservative 31; Mismatches 96; Indels 107; Gaps 13;

QY 16 LLLLSPLRGTPD-----CYFSHSPISSNEFKVFERELTDHLKD-YPVTV 62

[illegible]

QY 63 VNL-----QDEK-----HCKALMSFLAQR-W--IEQLKTVAGSKMOTLLE-----100

Db 197 AALETFEEVVCPEKLEIHPYHRICITLFPQNDWDKVALKTLVRYARLTLPESPSTH 256

QY 101 -DVNTEIHVTSCTFQPLPECL-----RFVQTNISHLKDTCTQLLALKPCIGKACQ 151

Db 257 SDLKELLESIKSCFFSLPSTIIAGARAFYYLAPSNQMHLLIVEPLQLLLEKPIVRTTL 316

```

152 N-----SRCLVQCQPBDSLLP----- 170
QY      | | | | | | | | | |

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DB 31 / KYSQVVKRPELFKNHKSFFLIASDSDI:CLKINILSKLLBQA ---NSSQILPELly 3/3

```

02 1/1 -----PRSPALLET-----PRKRQLLBBBLLBBPILVLLAAWGLR Z11
    :| | :| | | | | | | | | | | |

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DD 3/4 1 INSHFNF SVAS IAVNRLGDE FASAN ISMAFSCLNI LLLLLNASHNBLI V I EAASSUR 429

Search completed: August 6, 2002, 09:40:25
Job time: 216 sec

Job time: 216 sec

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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:46:19 ; Search time 16.81 Seconds
(without alignments) 532.077 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MVLAPAWSPNSILLILL.....WQARRRGELHPGVLPSP 231

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 50 summaries
SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1212.5	99.1	232	1 FLJL_MOUSE	P49772 mus musculus
2	768.5	62.8	235	1 FLJL_HUMAN	P49772 mus musculus
3	89.5	7.3	815	1 GBR2_HUMAN	O75899 homo sapien
4	89	7.3	815	1 AD15_MOUSE	O88833 mus musculus
5	87	7.1	816	1 AD15_RAT	O89400 r adam 15 p
6	84.5	6.9	1201	1 ATG3_HUMAN	O15072 homo sapien
7	84	6.9	1409	1 AEX3_CAEL	O02626 caenorhabdi
8	83.5	6.8	552	1 CSF1_MOUSE	P07141 mus musculus
9	83.5	6.8	2476	1 ZAN_PIG	O28983 sus scrofa
10	82.5	6.7	378	1 LEUK_RAT	P13838 ratu
11	80.5	6.6	335	1 APA4_MOUSE	P06728 mus musculus
12	80	6.5	195	1 INT_OVMO	P28172 ovibos mosc
13	79	6.5	1101	1 YAG_SCHPO	O09773 schistosac
14	78.5	6.4	122	1 YW2_MRCU	O50691 mycobacteri
15	78.5	6.4	1208	1 RCG4_HUMAN	O94761 homo sapien
16	78.5	6.4	3068	1 POG4_PEMVC	O01500 p genome po
17	78	6.4	224	1 CM35_HUMAN	O08708 homo sapien
18	78	6.4	806	1 SYB1_MOUSE	P47433 mycoplasma
19	78	6.4	908	1 YN61_YEAS	P42833 saccharomyc
20	77.5	6.3	266	1 HB2D_CANFA	P18470 canis fami
21	77.5	6.3	940	1 GBR2_RAT	O88871 ratu
22	76.5	6.3	222	1 YB95_METH	O27823 methanobact
23	76.5	6.3	336	1 VS09_ROTST	P03533 stiman 11 r
24	76.5	6.3	1296	1 ASAI_EMMPA	P11533 entrococcu
25	76.5	6.3	3660	1 DMD_CHICK	P11533 gallus gall
26	76	6.2	438	1 PR11_DROME	O24311 drosophila
27	76	6.2	977	1 EPP2_MOUSE	O03145 mus musculi
28	75.5	6.2	379	1 CYB_CANDR	P24952 camelus dro
29	75.5	6.2	577	1 TRBM_MOUSE	P15306 mus musculi
30	75.5	6.2	4543	1 LRPI_CHICK	P19157 gallus gall
31	75	6.1	433	1 AVR2_SCEUN	O94712 sceloporus
32	75	6.1	533	1 AVR2_HUMAN	P27037 homo sapien
33	75	6.1	732	1 KELT_HUMAN	P23276 homo sapien

34	75	6.1	758	1 VKGC_HUMAN	P38435 homo sapien
35	75	6.1	887	1 SM6B_RAT	O70141 ratu
36	74.5	6.1	326	1 VS09_ROTST	P08406 porcine rot
37	74.5	6.1	356	1 TRBM_BOVIN	P06579 bos taurus
38	74	6.1	326	1 VS09_ROTST	P11855 human rotav
39	74	6.1	326	1 VS09_ROTST	P12476 rhesus rota
40	74	6.1	448	1 BCN1_MOUSE	O88597 mus musculi
41	74	6.1	450	1 BCN1_HUMAN	O14457 homo sapien
42	74	6.1	478	1 BM3B_HUMAN	P55107 homo sapien
43	74	6.1	513	1 AVR2_BOVIN	O28043 bos taurus
44	74	6.1	513	1 AVR2_MOUSE	P27038 mus musculi
45	74	6.1	618	1 DIL3_HUMAN	O94717 homo sapien
46	74	6.1	811	1 TLRA_HUMAN	O28475 homo sapien
47	74	6.1	888	1 SM6B_HUMAN	O93163 homo sapien
48	74	6.1	1421	1 TIM_DROME	P49021 drosophila
49	73.5	6.0	415	1 TNR3_MOUSE	P50284 mus musculi
50	73.5	6.0	801	1 YEV7_YEAST	P40094 saccharomyc

ALIGNMENTS

RESULT	ID	FLJL_MOUSE	STANDARD	PRT	232 AA.
AC	P49772:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-OCT-2001 (Rel. 40, Last annotation update)				
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLR3 ligand)				
GN	FLR3LG OR FLR3L.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid-10090;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-94195428; PubMed-8145851;				
RX	Hannum C., Culpepper J., Campbell D., McLanahan T., Zurewski S.,				
RX	Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Loh J.,				
RX	Duda G., Marlin N., Peterson D., Menon S., Shattell A.,				
RX	Muench M., Kellner G., Nankawa R., Renwick D., Roncarolo M.G.,				
RX	Zlotnick A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.				
RT	*Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of				
RT	haematopoietic stem cells and is encoded by variant RNAs.;				
RL	Nature 368:643-648(1994).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-SUI/J.				
RX	MEDLINE-94084791; PubMed-7505204;				
RX	Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,				
RX	Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,				
RA	Spielt R.R., Fletcher F.A., Maraskovsky E., Farrah T.,				
RA	Forwerthe D., Williams D.E., Beckmann M.P.;				
RT	*Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase				
RT	receptor: a proliferative factor for primitive hematopoietic cells.;				
RT	Cell 75:1157-1167(1993).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-96032581; PubMed-7566977;				
RX	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,				
RA	Escobar S.;				
RT	*Structural analysis of human and murine flt3 ligand genomic loci.;				
RT	Oncogene 11:1165-1172(1995).				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-95124710; PubMed-7824267;				
RX	Lyman S.D., James L., Escobar S., Downey H., de Vries P.,				
RA	Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,				
RA	Cleveland L.S.;				
RT	*Identification of soluble and membrane-bound isoforms of the murine				
RT	flt3 ligand generated by alternative splicing of mRNAs.;				

OncoGene 10:149-157(1995).

RL [5]
 RP SEQUENCE FROM N.A.
 RA McClanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J.,
 RA Mattei M.-G., Rosnet O., Birnbaum D., Hannum C.,
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
 CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
 CC FACTORS AND INTERLEUKINS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
 CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
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 CC -----
 DR EMBL: U04807; AAA18000.1; -
 DR EMBL: L23636; AAA39436.1; -
 DR EMBL: U29875; AAA09951.1; -
 DR EMBL: U29875; AAA09952.1; -
 DR EMBL: S76459; AAB33069.1; -
 DR EMBL: S76461; AAB33070.1; -
 DR EMBL: U04024; AAA3306.1; -
 DR EMBL: U04024; AAA3306.1; -
 DR MGI: MGI:95560; Flt3l.
 DR Interpro: IPR004213; flt3_lig.
 DR Pfam: PF02947; flt3_lig; 1.
 DR Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.
 KW SIGNAL 1 26
 FT CHAIN 27 232
 FT DOMAIN 27 189
 FT TRANSSEM 190 210
 FT DOMAIN 211 232
 FT CARBOHYD 127 127
 FT CARBOHYD 152 152
 FT CARBOHYD 164 232
 FT VARSPLIC 164 232
 FT VARSPLIC 164 169
 FT VARSPLIC 170 232
 FT CONFLICT 141 141
 FT CONFLICT 198 198
 FT CONFLICT 198 198
 FT SEQUENCE 232 AA; 26141 MW; 3A3680D3CB69FBA6 CRC64;

Query Match 99.1%; Score 1212.5; DB 1; Length 232;
 Best Local Similarity 99.0%; Pred. No. 1e-99; 0; Indels 1; Gaps 1;
 Matches 231; Conservative 0; Mismatches 0;

QY 1 MTVALPAPMSNPSSLLDLLLSPCLNGPTDCTCFSHSPISSNKVFRELTDHLKDPVPT 60
 DB 1 MTVALPAPMSNPSSLLDLLLSPCLNGPTDCTCFSHSPISSNKVFRELTDHLKDPVPT 60
 DB 61 VAVVLDQEKCKALMSFLAQRIEQLKTVASCKMOTLLEDVNTFHHVTSCTQPIPEC 120
 QY 61 VAVVLDQEKCKALMSFLAQRIEQLKTVASCKMOTLLEDVNTFHHVTSCTQPIPEC 120
 DB 61 VAVVLDQEKCKALMSFLAQRIEQLKTVASCKMOTLLEDVNTFHHVTSCTQPIPEC 120
 QY 121 LRFVQTNISHLKDTCTQTLALPKICGAKQNFSCLEVOCPDSSTLLPRSPIALEAT 180
 DB 121 LRFVQTNISHLKDTCTQTLALPKICGAKQNFSCLEVOCPDSSTLLPRSPIALEAT 180
 QY 181 ELPPRRQQLLLLLLPITVLAAANGLMQARARRGELHREVPPLSPH 231
 DB 181 ELPPRRQQLLLLLLPITVLAAANGLMQARARRGELHREVPPLSPH 231

RESULT 2

FL3L_HUMAN STANDARD: PRT; 235 AA.

AC P49771;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLR3
 DE ligand).

DE FLR3L5.

CM FLR3L5.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
 [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-94195428; PubMed-8145851;
 RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
 RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
 RA Duda G., Matlana N., Peterson D., Menon S., Shanalelt A.,
 RA Muench M., Kelnar G., Nankawa R., Kennick D., Roncarolo M.G.,
 RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
 RT "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
 RT haematopoietic stem cells and is encoded by variant RNAs.";
 RN Nature 368:643-648(1994).
 [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-94235842; PubMed-8180375;
 RA Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
 RA Escobar S.S., Downey H., Spielt R.R., Beckmann M.P., McKenna H.J.;
 RT "Cloning of the human homologue of the murine flt3 ligand: a growth
 RT factor for early hematopoietic progenitor cells.";
 RN Blood 83:2795-2804(1994).
 [3]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

RX MEDLINE-96032581; PubMed-7566977;
 RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.;
 RT "Structural analysis of human and murine flt3 ligand genomic loci.";
 RL OncoGene 11:1165-1172(1995).

CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
 CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
 CC FACTORS AND INTERLEUKINS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
 CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.

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DR EMBL: U04806; AAA17999.1; -
 DR EMBL: U03858; AAA19825.1; -
 DR EMBL: U29874; AAA09949.1; -
 DR EMBL: U29874; AAA09950.1; -
 DR MIM: 600007; -
 DR Interpro: IPR004213; flt3_lig.
 DR Pfam: PF02947; flt3_lig; 1.
 DR Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.

KW SIGNAL 1 26
 FT CHAIN 27 235
 FT DOMAIN 27 184
 FT TRANSSEM 185 205
 FT DOMAIN 206 235
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

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FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

FT VARSPLIC 161 176

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FT      (IN SOLUBLE ISOFORM).
FT      MISSING (IN SOLUBLE ISOFORM).
FT      VARSPLIC 179 235
FT      CONFLICT 72 72 G -> A (IN REF. 1).
SQ      SEQUENCE 235 AA; 26416 MW; 73b95b693b4CECF CRC64;

Query Match      62.8%: Score 768.5; DB 1; Length 235;
Best Local Similarity 70.3%: Pred No. 1,2e-60;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

OY      1 MVLVLPAMSPNSLLLLLSPLCLGRTPDCYFSSPISSNFKYKRELTHLKDYPVT 60
DB      1 MVLVLPAMSP-PTLLLLLSGLSGTODCSFQHSPISSDPAVKIRLSDYLLDDYPT 59
OY      61 VAVNLOEKKCALMSLFLAQRWIEQLKIVASKKQMTLEEDVNTFHPVTSCTPCLPEC 120
DB      60 VASNLQDEELCGMLRVLVAQRMERLKTIVASKMOGLERNTLHVTCAFPQPPSC 119
OY      121 LRFVQNIISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPTALEAT 180
DB      120 LRFVQNIISHLKDTCTQLALKPCIGKACQNFSCLEVOCPDSSSTLLPPRSPTALEAT 177
OY      181 ELDEPRPRQLLLLLPLTVLLAAAGLRRORARR----GELHPGVLEP 228
DB      178 APRAPQP-LLLLPLPVLGALLAAKCLHMQRTRRTRPRGEGYPPVPSP 227

RESULT 3
GBR2_HUMAN
ID      GBR2_HUMAN STANDARD; PRT; 941 AA.
AC      075899; 075974; 075975; 09UNSR; Q9UNR1; Q9P1R2;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DE      Gamma-aminobutyric acid type B receptor, subunit 2 precursor (GABA-B
DE      51) (GPR 51) (HG20).
GN      GABBR2 OR GPR51.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 2A).
RX      MEDLINE=99087321; PubMed=9872316;
RA      White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA      Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT      "Heterodimerization is required for the formation of a functional
RT      GABA(B) receptor.";
RL      Nature 396:679-682(1998).
RN      [2]
RP      PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RX      MEDLINE=20193514; PubMed=10727622;
RA      Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT      "Distribution of the GABA(B) receptor subunit gb2 in rat CNS.";
RL      Brain Res. 860:41-52(2000).
RN      [3]
RP      SEQUENCE FROM N.A. (ISOFORM 2A).
RA      Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G.,
RA      Herzog H.;
RT      "Cloning and characterization of a novel human GABA-B receptor subtype
RT      with high affinity for GABA and low affinity for baclofen.";
RL      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN      [4]
RP      SEQUENCE FROM N.A. (ISOFORM 2A).
RC      TISSUE=Hippocampus;
RA      Borowsky B., Laz T., Gerald C.;
RL      Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A. (ISOFORM 2A).
RC      TISSUE=Fetal brain;

RX      MEDLINE=99189236; PubMed=10087195;
RA      Ng G.Y.K., McDonald T., Bonner T., Rigby M., Heavens R., Whiting P.,
RA      Chateaufort A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
RA      O'Neill G.P., Liu Q.;
RT      "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
RT      receptors expressed predominantly in nervous tissues and mapped
RT      proximal to the hereditary sensory neuropathy type 1 locus on
RT      chromosome 9";
RL      Genomics 56:288-295(1999).
RN      [6]
RP      SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
RC      TISSUE=Brain;
RX      MEDLINE=99263199; PubMed=10328880;
RA      Martin S.C., Russek S.J., Farb D.H.;
RT      "Molecular identification of the human GABABR2: cell surface
RT      expression and coupling to adenylyl cyclase in the absence of
RT      GABABR1";
RL      Mol. Cell. Neurosci. 13:180-191(1999).
RN      [7]
RP      R1A-R2 INTERACTION.
RX      MEDLINE=99175124; PubMed=10075644;
RA      Ng G.Y.K., Clark J., Coulombe N., Elhier N., Hebert T.E., Sullivan R.,
RA      Kargman S., Chateaufort A., Tsukamoto N., McDonald T., Whiting P.,
RA      Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
RA      Bonner T.I., O'Neill G.P.;
RT      "Identification of a GABAB receptor subunit, gb2, required for
RT      functional GABAB receptor activity.";
RL      J. Biol. Chem. 274:7607-7610(1999).
RN      [8]
RP      R1A-R2 INTERACTION.
RX      MEDLINE=20237752; PubMed=10773016;
RA      Sullivan R., Chateaufort A., Coulombe N., Kolakowski L.F. Jr.,
RA      Johnson M.P., Hebert T.E., Elhier N., Belsey M., Welters K.,
RA      Abramovitz M., O'Neill G.P., Ng G.Y.K.;
RT      "Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))
RT      receptors with truncated receptors and metabotropic glutamate
RT      receptor 4 supports the GABA(B) heterodimer as the functional
RT      receptor.";
RL      J. Pharmacol. Exp. Ther. 293:460-467(2000).
RN      [9]
RP      FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC      MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC      STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC      INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC      INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC      FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
CC      GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC      HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC      GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC      INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC      LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC      SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC      POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC      ANTINOCICEPTION.
CC      [10]
CC      SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC      IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC      HAPPEN.
CC      [11]
CC      COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC      PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC      PLASMA MEMBRANE.
CC      [12]
CC      ALTERNATIVE PRODUCTS: 3 ISOFORMS: 2A (SHOWN HERE), 2B AND 2C; ARE
CC      PRODUCED BY ALTERNATIVE SPLICING.
CC      [13]
CC      TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
CC      CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
CC      TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
CC      CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.
CC      [14]
CC      WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
CC      [15]
CC      -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
CC      MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC      [16]
CC      -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC      [17]
CC      GABA-B RECEPTOR SUBFAMILY.
CC      [18]
CC      -----
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DR EMBL: AF012188; CAA09942.1; -
DR EMBL: AF056085; AAC63228.1; -
DR EMBL: AF095723; AAC63383.1; -
DR EMBL: AF095724; AAC63384.1; -
DR EMBL: AF095784; AAD30389.1; -
DR EMBL: AF074483; AAD03336.1; -
DR EMBL: AF069755; AAC99345.1; -
DR EMBL: AF099033; AAD45867.1; -
DR InterPro: IPR001828; ANF_Receptor.
DR InterPro: IPR00337; GPCR_Mgr.
DR Pfam: PF00003; 7tm_3; 1.
DR Pfam: PF01094; ANF_receptor; 2.
DR PRINTS: PFO0248; GPCRMR.
DR PRINTS: PFO1176; GABABRECEPT.
DR PRINTS: PFO1177; GABAB1RECEPT.
DR PRINTS: PFO1178; GABAB2RECEPT.
DR PROSITE: PS00979; G_PROTEIN_RECPT_F3_1; FALSE_NEG.
DR PROSITE: PS00980; G_PROTEIN_RECPT_F3_2; FALSE_NEG.
DR PROSITE: PS00981; G_PROTEIN_RECPT_F3_3; FALSE_NEG.
DR PROSITE: PS50259; G_PROTEIN_RECPT_F3_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Postsynaptic membrane; Collod coll; Alternative splicing;

FT	SIGNAL	1	41	POTENTIAL.
FT	CHAIN	42	941	GAMMA-AMINOBUTYRIC ACID TYPE B RECEPTOR, SUBUNIT 2.
FT	DOMAIN	42	483	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	484	504	I (POTENTIAL).
FT	DOMAIN	505	522	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	523	543	II (POTENTIAL).
FT	DOMAIN	544	551	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	552	572	III POTENTIAL.
FT	DOMAIN	573	597	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	598	618	IV (POTENTIAL).
FT	DOMAIN	619	654	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	655	675	V (POTENTIAL).
FT	DOMAIN	676	691	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	692	712	VI (POTENTIAL).
FT	DOMAIN	713	720	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	721	741	VII (POTENTIAL).
FT	DOMAIN	742	941	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	781	819	COILED COIL (POTENTIAL).
FT	CARBOHYD	90	90	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	389	389	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	404	404	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	453	453	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	902	929	MISSING (IN ISOFORM 2B).
FT	VARSPPLIC	929	941	HYPERSPVMVSGL -> TLTGRCVCCRNVSQCEAGHHG WPLATTMALRMTGRGRGLGT (IN ISOFORM 2C).
FT	VARIANT	628	628	Y -> F.
FT	VARIANT	659	869	/FtId=VAR_010148.
FT	VARIANT	869	869	T -> A.
FT	CONFLICT	6	6	/FtId=VAR_010149.
FT	CONFLICT	12	12	S -> R (IN REF. 5).
FT	CONFLICT	424	424	P -> R (IN REF. 5).
FT	CONFLICT	941 AA:	105821 MM:	G -> E (IN REF. 3).
FT	SEQUENCE	941 AA:	105821 MM:	09GLF73DB0673C5D CRC64;

Query Match	7.38;	Score 89.5;	DB 1;	Length 941;
Best Local Similarity	49.0%;	Pred. No. 3;		
Matches	24;	Conservative	0;	Mismatches 16; Indels 9; Gaps 2;

QY 183 PEPRRQLLLLLLLPTLVLLAAWGLRWQRARRRGELHPVLPSPH 231
| | | | | | | | | | | | | | | | | |
'

RESULT	4
AD15_MOUSE	
ID	AD15_MOUSE
STANDARD;	
PRT;	815 AA

DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin)
DE (Metargidin) (AD55).
DE (Metargidin) (AD55).
GN ADAM15 OR MDC15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1] _____
RP SEQUENCE FROM N.A., AND INTRACELLULAR MATURATION.
RP TISSUE=Lung;
RC MEDLINE=98421554; PubMed=97488307;
RA Lum L., Reid M.S., Blobel C.P.;
RT "Intracellular maturation of the mouse metalloprotease disintegrin MDC15.";
J. Biol. Chem. 273:26236-26247(1998).

RP SEQUENCE FROM N.A.
RC TISSUE=Myeloid; and Myeloma;
RA Shimizu E., Higuchi Y., Matsura K., Hijiya N., Yamamoto S.;
RT "Structure of the mouse ADAM 15 (AD56) gene."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP INTERACTIONS WITH ENDOPHILIN I AND SORTING NEXIN 9.
RX MEDLINE=20002705; PubMed=10531379;
RA Howard L., Nelson K.K., Maciewicz R.A., Biobel C.P.;
RT "Interaction of the metalloprotease disintegrins MOC9 and MD015 with
the sh3 domain-containing proteases, endophilin I and SH3p11."
RL J. Biol. Chem. 274:31693-31699(1999).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-SURFACE PROTEOLYSIS, CELL
ADHESION OR INTRACELLULAR PROTEIN MATURATION.
CC -1- COPACITOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH INTERLIN ALPHA-V-BETA3, ENDOPHILIN I AND
SORTING NEXIN 9. ENDOPHILIN I AND SORTING NEXIN 9 PREFERENTIALLY
CC BIND THE PRECURSOR BUT NOT THE PROCESSED FORM OF ADAM15,
SUGGESTING THAT THE INTERACTION OCCURS IN A SECRETORY PATHWAY
CC COMPARTMENT PRIOR TO THE MEDIAL GOLGI.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THE MAJORITY OF THE
PROTEIN IS LOCALIZED IN A PERINGOLAR COMPARTMENT WHICH MAY
CC CORRESPOND TO THE TRANS-GOLGI NETWORK OR THE LATE ENDSOME. THE
PRO-PROTEIN IS THE MAJOR DETECTABLE FORM ON THE CELL SURFACE,
CC WHEREAS THE MAJORITY OF THE PROTEIN IN THE CELL IS PROCESSED.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, BRAIN, LUNG, AND
CC KIDNEY. EXPRESSED AT LOWER LEVELS IN SPLEEN, LIVER, TESTIS AND
CC MUSCLE.
CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
CC SORTING NEXIN 9.
CC -1- DOMAIN: DISENTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA-V-BETA3 (BY
CC SIMILARITY).
CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE. AN
CC ADDITIONAL MEMBRANE PROXIMAL SITE OF CLEAVAGE AFFECTS A SMALL
CC PERCENTAGE OF THE PROTEIN AND RESULTS IN DISULFIDE-LINKED
CC FRAGMENTS. THE PRO-DOMAIN IS APPARENTLY CLEAVED IN SEVERAL
CC POSITIONS THAT ARE N-TERMINAL OF THE FURIN CLEAVAGE SITE.
CC -1- PTM: MAY BE PARTIALLY NITRYLATED.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 DISENTEGRIN DOMAIN.

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CC

DR PROSITE; PS0092; TSP1; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 KM Hydrolase; Metalloprotease; zinc; Signal; Glycoprotein; Zymogen;
 KM Repeat; Extracellular matrix; Heparin-binding.

FT SIGNAL 1 1
 FT PROPEP <1 2
 FT CHAIN 245 245
 FT METAL 246 1201
 FT ACT_SITE 394 394
 FT METAL 395 395
 FT METAL 398 398
 FT METAL 404 404
 FT METAL 466 546
 FT DOMAIN 547 603
 FT DOMAIN 604 708
 FT DOMAIN 709 840
 FT DOMAIN 841 898
 FT DOMAIN 899 961
 FT DOMAIN 962 1013
 FT DOMAIN 242 245
 FT CARBOHYD 79 79
 FT CARBOHYD 115 115
 FT CARBOHYD 238 238
 FT CARBOHYD 341 341
 FT CARBOHYD 471 471
 FT CARBOHYD 810 810
 FT CARBOHYD 938 938
 SQ SEQUENCE 1201 AA; 135113 MW; D54EA92BD506A3AA CRC64;

Query Match 6.9%; Score 84.5; DB 1; Length 1201;
 Best Local Similarity 21.9%; Pred. No. 11;
 Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10;

QY 40 SNFKVFRRLTDLKLDYPTVAVNLQDEKHKALMSFLAQRMLEQKTVAGSK----- 94
 DB 872 SDKKVHRSFCSEANKKPKIRRMCMNQECTH-----PLWVAEMHCHRTGSSGYQLRT 926
 QY 95 ---MOTLLEVNTEHFV-----TSCIFQPLP-----ELKRYV--QTINSH 130
 DB 927 VRCLOPLDSTNSVSKYCMGDRPESRRPCRRVPCPQWKGTGWSSECVTGEQTEVRQ 986
 QY 131 LT-----KDTCTQLLAKPCIGKAC-----QNEFRCLEAYQ 161
 DB 987 VLCRADHDCGKESVSRACQLPNCDEPCLGDKSLPCOMEVLARYCSIPGNKIKCCESC 1046
 QY 162 QPSSSTLPPRSPIALETEL-----PEPPRQLLLLLLP 198
 DB 1047 SKRST-LRP--PYLLEAETHDDVYSNPSDLPRSLVMPSTSLVP 1087

RESULT 7
 AEX3_CAEEL STANDARD; PRT; 1409 AA.
 AC 002626; 027467;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Regulator of presynaptic activity aex-3.
 GN AEX-3 OR CO2H7.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA MEDLINE=97282461; PubMed=9136770;
 RA Iwasaki K., Staunton J., Saifee O., Monet M., Thomas J.H.;
 RT "aex-3 encodes a novel regulator of presynaptic activity in C.
 elegans";
 RL Neuron 18:613-622(1997).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Iwasaki K., Toyonaga R.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP INTERACTION WITH CAB-1.
 RX MEDLINE=20428446; PubMed=10970871;
 RA Iwasaki K., Toyonaga R.;
 RT "The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
 in synaptic transmission";
 RL EMBL J 19:4806-4816(2000).
 CC -1- FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) FOR RAB3. MAY
 REGULATE TWO DIFFERENT PATHWAYS FOR NEURAL ACTIVITIES.
 CC -1- SUBUNIT: BINDS TO CAB-1.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS.
 CC -1- SIMILARITY: CONTAINS 1 DENN DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC EMBL: U93842; AAB52421.1; -;
 DR EMBL: U49945; AAC47926.1; -;
 DR WormBep: C02H7.3; CEI6806.
 DR InterPro: IPR001194; DENN.
 DR Pfam: PF02141; DENN; 1.
 KW Guanine-nucleotide releasing factor.
 FT DOMAIN 216 364
 FT DOMAIN 604 632
 SQ SEQUENCE 1409 AA; 157458 MW; 2DDE6395AC963313 CRC64;

Query Match 6.9%; Score 84; DB 1; Length 1409;
 Best Local Similarity 23.9%; Pred. No. 14;
 Matches 54; Conservative 31; Mismatches 73; Indels 68; Gaps 13;

QY 4 LAPAMSPNSLLLLLLSPCLRGTPDCYFSHPISNFKVFRRL-TDHLKDYPTVA 62
 DB 317 LTPAVPMSAE-QLLAPPLFLIGVPSFFNHR-----KIRELPSDVIYDLD-TNC 365
 QY 63 VNLQDEKHKALMSFL-----AQRMLEQKTVAGSKMOTLLEDVNTE----- 105
 DB 366 LQVPPD-----LITPDLPEDATHLKERUK-AIKMTTMTVDNDSVTADDEGIDI 416
 QY 106 -----IHFTVSC-----TEOPLPECLRFVQTNISHLKDYCTQLALK 143
 DB 417 DSDVDACRVAMVQFNSAVFGNFSEHTRRLTLPVPVYSIQTDSFLRSRPOCTQLIT-D 475
 QY 144 PCIGKACONEFRCLEVOCA-PDSSTLPPRSPIALETELPEPPR 188
 DB 476 LCHTQAVETFAEC-----CLCPKNETFV--RVQAGIESAEOYGDKPK 515

RESULT 8
 CSFL_MOUSE STANDARD; PRT; 552 AA.
 ID CSFL_MOUSE
 AC P07141;
 DT 01-APR-1998 (Rel. 07, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Macrophage colony stimulating factor-1 precursor (CSF-1) (M-CSF).
 GN CSF1 OR CSFM.
 OS Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090, 10116;
 RN [1]

RP SEQUENCE FROM N.A.
 RC MEDLINE-87174763; PubMed-3494232;
 RA Delamarter J.F., Hession C., Semon D., Gough N.M., Rothenbuhler R.,
 RT Mermod J.-J.;
 RT "Nucleotide sequence of a cDNA encoding murine CSF-1
 (Macrophage-CSF).";
 RL Nucleic Acids Res. 15:2389-2390(1987).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-88320507; PubMed-2457916;
 RA Ladner M.B., Martin G.A., Noble J.A., Wittman V.P., Warren M.K.,
 RT McGrogan M., Stanley E.R.;
 RT "cDNA cloning and expression of murine macrophage colony-stimulating
 factor from 1929 cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:6706-6710(1988).
 RN
 RP SEQUENCE OF 1-100 FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-8714732; PubMed-3493488;
 RA Rajavashisth T.B., Eng R., Shaddock R.K., Waheed A., Ben-Avram C.M.,
 RA Shively J.E., Lusis A.J.;
 RT "Cloning and tissue-specific expression of mouse macrophage colony-
 stimulating factor mRNA";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1157-1161(1987).
 RN
 RP SEQUENCE OF 33-57.
 RC SPECIES-MOUSE;
 RX MEDLINE-85242709; PubMed-3925458;
 RA Ben-Avram C.M., Shively J.E., Shaddock R.K., Waheed A.,
 RA Rajavashisth T.B., Lusis A.J.;
 RT "Amino-terminal amino acid sequence of murine colony-stimulating
 factor 1";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4486-4489(1985).
 RN
 RP SEQUENCE FROM N.A.
 RC SPECIES-RAT; STRAIN-WISTAR; TISSUE-Muscle;
 RX MEDLINE-93363632; PubMed-8357831;
 RA Borczyk A.G., Lemorund J., Guiller M., Lebovitch S.A.;
 RT "Isolation and characterization of a cDNA clone encoding for rat
 CSF-1 gene. Post-transcriptional repression occurs in myogenic
 differentiation";
 RL Biochim. Biophys. Acta 1174:143-152(1993).
 RN
 RP SEQUENCE OF 1-13 FROM N.A.
 RC SPECIES-MOUSE;
 RX MEDLINE-91340149; PubMed-1874443;
 RA Harrington M.A., Edenberg H.J., Saxman S.M., Pedigo L.M., Daub R.,
 RA Brockmeyer H.E.;
 RT "Cloning and characterization of the murine promoter for the colony-
 stimulating factor-1-encoding gene";
 RL Gene 102:165-170(1991).
 CC
 CC - FUNCTION: GRANDLOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
 CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
 CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
 CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES.
 CC
 CC - FUNCTION: THIS CSF INDICES MACROPHAGES
 CC - SUBUNIT: HOMODIMER, LINKED BY THREE DISULFIDE BONDS.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X05010; CAA28660.1; -
 DR EMBL; M21952; AAA37481.1; -
 DR EMBL; M21149; AAA37482.1; -
 DR EMBL; M15692; AAA37480.1; -
 DR EMBL; M84361; AAA03032.1; -

DR EMBL; M81316; AAA19856.1; -
 DR PIR; A23166; A23166.
 DR PIR; A26575; A26575.
 DR PIR; A31401; A31401.
 DR MCD; MG1:1339753; CSFL.
 KW cytokine; Growth factor; glycoprotein; signal.
 FT SIGNAL 1 32
 FT CHAIN 33 552
 FT DISULFID 63 63
 FT DISULFID 39 122
 FT DISULFID 80 171
 FT DISULFID 134 178
 FT DISULFID 189 189
 FT DISULFID 191 191
 FT CARBOHYD 107 107
 FT CARBOHYD 154 154
 FT CARBOHYD 172 172
 FT VARIANT 292 292
 FT VARIANT 345 345
 FT VARIANT 3 3
 FT CONFLICT 6 6
 FT CONFLICT 7 8
 FT CONFLICT 246 246
 FT CONFLICT 246 246
 SQ SEQUENCE 552 AA; 60648 MW; 3886D72D70E770AF CRC64;
 Query Match 6.8%; Score 83.5; DB 1; Length 552;
 Best Local Similarity 23.2%; Pred. No. 5.5;
 Matches 54; Conservative 36; Mismatches 94; Indels 49; Gaps 12;
 QY 12 SLLILLLLPCLRLGTPDCYFSHPISNFKVKEKRETLHLKDYPTAVNLDEKH-70
 DB 18 SRLVLCLMSRSIAKVESEHSCSHMGHGLKV-IQOLIDSQM-ETSCQIAFEFVDEQL-75
 QY 71 ----CKALMSFLAQRRIEDL-----KYVAGSKMQLLEDVTHHTFTSCFQPLP-118
 DB 76 DDPVCYKKAFFLVQDITIDETMRKDNTPNANATERLOELSNLN-----SCFTDYE-128
 QY 119 E----CLR-EVQT-----NISHLKDTCTDLAKPCIGKACON-FSRG--LEVOGCPD-164
 DB 129 EQNKACVETREHPEQLLEKIKFNEFKNLLEKDMNIFTKCNNSFKCSRVVVRKP-188
 QY 165 SSTLLPRSPALEATELEPPRRQQLLLPLTVLLAAMGLRGRRAR-217
 DB 189 CNCYPRATPSDDPASAPHPAP-----SWAPLA-----GLAMDDSOR-228
 RESULT 9
 ZAN_PIG STANDARD; PRT: 2476 AA.
 ID ZAN_PIG
 AC Q28983;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Zonadhesin precursor.
 GN ZAN.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 CC NCBI_TaxID=9823;
 CC
 CC [1]
 CC SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890;
 CC 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656;
 CC 1658-1667; 1777-1795 AND 1914-1921.
 CC STRAIN-MEISHAN; TISSUE-Testis;
 CC MEDLINE-96064658; PubMed-7592795;
 RA Hardy D.M., Gaiders D.L.;
 RT "A sperm membrane protein that binds in a species-specific manner to
 RT the egg extracellular matrix is homologous to von Willebrand
 RT factor";
 RL J. Biol. Chem. 270:26025-26028(1995).
 CC - FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA
 CC OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR

SIGNALING.

-1- SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).

-1- TISSUE SPECIFICITY: IN TESTIS, PRIMARILY IN HAPLOID SPERMATIDS. NOT IN LUNG, LIVER, HEART, SPLEEN, BRAIN, KIDNEY, EPIDIDYMIS.

-1- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.

-1- DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.

-1- DOMAIN: THE WMPD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).

-1- PTM: THE MAM DOMAINS AND THE MUCIN-LIKE DOMAINS ARE MISSING FROM THE ZONAADHESIN THAT BINDS TO THE EGG EXTRACELLULAR MATRIX. PROCESSING MIGHT OCCUR DURING SPERM MATURATION AND/OR CAPACITATION.

-1- SIMILARITY: CONTAINS 2 MAM DOMAINS.

-1- SIMILARITY: CONTAINS 4.5 WMPD DOMAINS.

-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

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CC EMBL; U40024; AAC48486.1; .

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR000998; MAM.

DR InterPro: IPR002919; TIL.

DR InterPro: IPR003328; TILA.

DR InterPro: IPR001007; VMFC.

DR InterPro: IPR001846; VWD.

DR Pfam: PF00629; MAM; 2.

DR Pfam: PF01826; TIL; 5.

DR Pfam: PF02345; TILA; 5.

DR Pfam: PF00094; VWD; 4.

DR SMART: SM00181; EGF; 1.

DR SMART: SM00137; MAM; 1.

DR SMART: SM00214; WMC; 2.

DR SMART: SM00216; VWD; 4.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 4.

DR PROSITE: PS00740; MAM_1; 1.

DR PROSITE: PS00650; MAM_2; 2.

KW Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion; Repeat.

KW Repeat.

FT SIGNAL 1 29

FT CHAIN 30 2476

FT DOMAIN 30 2418

FT TRANSMEM 2419 2439

FT DOMAIN 2440 2476

FT DOMAIN 31 144

FT DOMAIN 147 312

FT DOMAIN 319 687

FT DOMAIN 688 799

FT DOMAIN 800 1184

FT DOMAIN 1185 1573

FT DOMAIN 1574 1968

FT DOMAIN 1969 2370

FT DOMAIN 2366 2402

FT DISULFID 2370 2381

FT DISULFID 2375 2390

FT DISULFID 2392 2401

FT CARBOHYD 109 109

FT CARBOHYD 269 269

FT CARBOHYD 735 735

FT CARBOHYD 738 738

FT CARBOHYD 833 833

POTENTIAL.

ZONAADHESIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

MAM 1.

MAM 2.

53 X HEPTAPEPTIDE REPEATS (APPROXIMATE) (MUCIN-LIKE DOMAIN).

WMPD 1 (PARTIAL).

WMPD 2.

WMPD 3.

WMPD 4.

WMPD 5.

EGF-LIKE.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1154 1154 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1329 1329 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1448 1448 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1544 1544 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1544 1544 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1596 1596 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1654 1654 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1843 1843 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 1965 1965 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2122 2122 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2165 2165 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2178 2178 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2329 2329 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 2359 2359 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 823 823 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 923 923 C -> V (IN REF. 1; AA SEQUENCE).

FT CONFLICT 965 965 S -> Y (IN REF. 1; AA SEQUENCE).

FT CONFLICT 1241 1241 W -> K (IN REF. 1; AA SEQUENCE).

SO SEQUENCE 2476 AA; 270364 MW; A1386903756548C CRC64;

Query Match Best Local Similarity 30.6%; Score 83.5; DB 1; Length 2476; Pred. No. 30;

Matches 26; Conservative 12; Mismatches 32; Indels 15; Gaps 3;

QY 144 PCIGKACQNFSCLE-----VQCC-----PDSSTLLPPRSPLADATELPEPRQILL 193

DB 2369 PCLNCPQNDGRCRREGGTHFTCECELGYGGLCT-----EPKGVPSPKPKPEASNVAIL 2423

QY 194 LLLPLPTVLAAAMGLRWRARRR 218

DB 2424 GMLMPVLVLPAYTRVSRRRRRR 2448

RESULT 10

LEUK_RAT

ID LEUK_RAT STANDARD: PRT: 378 AA.

AC P13838:

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Leukostalin precursor (Leucocyte stialoglycoprotein) (Stialophorin)

DE (CD43) (W3/13 antigen) (Fragment).

GN SPN.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

ON NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Thymocytes;

RX MEDLINE=8816646; PubMed=2965006;

RA Killen N., Barclay A.N., Willis A.C., Williams A.F.;

RT "The sequence of rat leukostalin (W3/13 antigen) reveals a molecule with O-linked glycosylation of one third of its extracellular amino acids."

RL EMBO J. 6:4029-4034(1987).

CC -1- FUNCTION: ONE OF THE MAJOR GLYCOPROTEINS OF THYMOCYTES AND T LYMPHOCYTES. PLAYS A ROLE IN THE PHYSICO-CHEMICAL PROPERTIES OF THE T-CELL SURFACE AND IN LECTIN BINDING. PRESENTS CARBOHYDRATE LIGANDS TO SELECTINS. HAS AN EXTENDED ROD-LIKE STRUCTURE THAT COULD PROTRUDE ABOVE THE GLYCOCALYX OF THE CELL AND ALLOW MULTIPLE

CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.

CC -1- TISSUE SPECIFICITY: CELL SURFACE OF THYMOCYTES, T LYMPHOCYTES, NEUTROPHILS, PLASMA CELLS AND MELOMAS.

CC -1- PTM: HAS A HIGH CONTENT OF SIALIC ACID AND O-LINKED CARBOHYDRATE STRUCTURES.

CC -----

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FT REPEAT 225 246 9.
FT REPEAT 247 268 10.
FT REPEAT 269 286 11.
FT REPEAT 287 308 12.
FT REPEAT 309 330 13.
FT DOMAIN 366 389 GLU/GLN-RICH.
FT VARIANT 382 385 MISSING (IN SOME STRAINS).
FT CONFLICT 15 15 MISSING (IN REF. 1).
FT CONFLICT 63 63 O -> K (IN REF. 1).
FT CONFLICT 207 207 E -> R (IN REF. 1).
FT CONFLICT 288 288 S -> A (IN REF. 1).
FT CONFLICT 294 295 RQ -> KA (IN REF. 1).
FT CONFLICT 315 316 NK -> GG (IN REF. 1).
SQ SEQUENCE 395 AA; 45029 MW; 5FE27D0236226257 CRC64;

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Query Match 6.6%; Score 80.5; DB 1; Length 395;
Best Local Similarity 21.1%; Pred. No. 6.9; Mismatches 69; Indels 27; Gaps 6;
Matches 37; Conservative 42;

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QY 11 NSLLLLLLSPCLR-----GTPDCYFSPSSNFKVF---REITDHL--LK 55
DB 147 NNGQEMKQLQPLVYQRMQTIKENVDNLHFSMPPLATNLKDKENRMEELKGLTPRAN 206
QY 56 DYPVAVANLQDEKCKRLNSFLAQKRIEOLKTVASKMOGLLEVDNTEIHVYTSCTFQ 115
DB 207 ELKATIDNLEDRSLAPLVGVQEKLNHMEGLA-FQMKKNMEELQTRV---SAKID 261
QY 116 PLPECLRFQVQINSHLKDCTQTLALKPCIGKACQNFSCLEVOQCPDSSTLIP 170
DB 262 QL-----QKNLAPLVEDVQSKVKGNEGLQKLEDLNRLQLEQVEFRTYEP 309

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RESULT 12
INT_OVIMO STANDARD; PRT; 195 AA.
AC P28172;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interferon tau precursor (IFN-tau) (Trophoblast protein-1) (TP-1) (Trophoblastin) (Antileuteolysin) (Trophoblast antileuteolytic protein).
GN IFN OR IFN.
OS Ovis aries moschatus (Muskhox).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovidos.
OC NCBI_TaxID=37176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92242937; PubMed=1374107;
RA Legman D.W., Roberts R.M.;
RT "Genes for the trophoblast interferons in sheep, goat, and musk ox and distribution of related genes among mammals.";
RL J. Interferon Res. 12:1-11(1992).
RN [2]
RP REVIEW.
RX MEDLINE=99081096; PubMed=9865498;
RA Marital J.L., Chene N.M., Huynh L.P., L'Hardon R.M., Reinaud P.B., Gullonnet M.W., Charlier M.A., Charigny S.Y.;
RT "IFN-tau: a novel subtype I IFN1. Structural characteristics, non-ubiquitous expression, structure-function relationships, a pregnancy hormonal embryonic signal and cross-species therapeutic potentialities.";
RL Biochimie 80:755-777(1998).
-1- FUNCTION: PARACRINE HORMONE PRIMARILY RESPONSIBLE FOR MATERNAL RECOGNITION OF PREGNANCY. INTERACTS WITH ENDOMETRIAL RECEPTORS, PROBABLY TYPE I INTERFERON RECEPTORS, AND BLOCKS ESTROGEN RECEPTOR EXPRESSION, PREVENTING THE ESTROGEN-INDUCED INCREASE IN OXYTOCIN RECEPTOR EXPRESSION IN THE ENDOMETRIUM. THIS RESULTS IN THE SUPPRESSION OF THE PULSATILE ENDOMETRIAL RELEASE OF THE LUTEOLYTIC HORMONE PROSTAGLANDIN F2-ALPHA, HINDERING THE REGRESSION OF THE CORPUS LUTEUM (LUTEOLYSIS) AND THEREFORE A RETURN TO OVARIAN

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CC CYCLOTICITY. THIS, AND A POSSIBLE DIRECT EFFECT OF IFN-TAU ON
CC PROSTAGLANDIN SYNTHESIS, LEADS IN TURN TO CONTINUED OVARIAN
CC PROGESTERONE SECRETION, WHICH STIMULATES THE SECRETION BY THE
CC ENDOMETRIUM OF THE NUTRIENTS REQUIRED FOR THE GROWTH OF THE
CC CONCEPTUS. IN SUMMARY, DISPLAYS PARTICULARLY HIGH ANTIVIRAL AND
CC ANTIPROLIFERATIVE POTENCY CONCURRENTLY WITH PARTICULAR WEAK
CC CYTOTOXICITY, HIGH ANTILEUTEOLYTIC ACTIVITY AND IMMUNOMODULATORY
CC PROPERTIES. IN CONTRAST WITH OTHER IFNS, IFN-TAU IS NOT VIRALLY
CC INDUCIBLE.
CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE UTERINE LUMEN.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY AND EXCLUSIVELY EXPRESSED IN
CC THE MONONUCLEAR CELLS OF THE EXTRA-EMBRYONIC TROPHOCTODERM.
CC -1- DEVELOPMENTAL STAGE: MAJOR SECRETORY PRODUCT SYNTHESIZED BY THE
CC CONCEPTUS DURING A VERY SHORT PERIOD IN EARLY PREGNANCY.
CC -1- MISCELLANEOUS: IFN-TAU GENES ARE INTERLOUS. THEY EVOLVED FROM
CC IFN-OMEGA GENES IN THE RUMINANTIA SUBORDER AND HAVE CONTINUED TO
CC DUPLICATE INDEPENDENTLY IN DIFFERENT LINEAGES OF THE RUMINANTIA.
CC THEY ENCODE FOR PROTEINS VERY SIMILAR IN SEQUENCE BUT WITH
CC DIFFERENT BIOLOGICAL POTENCY AND PATTERN OF EXPRESSION.
CC -1- SIMILARITY: BELONGS TO THE INTERFERON ALPHA, BETA AND DELTA
CC FAMILY. IFN-ALPHA1 SUBFAMILY.
CC -----
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CC -----
DR EMBL: M73244; AAA31583.1; -.
DR HSSP: P01563; 2HIE.
DR InterPro: IPR000471; Interferon_abd.
DR Pfam: PF00143; Interferon_1.
DR PRINTS: PR00266; INTERFERONAB.
DR ProDom: PD000550; Interferon_abd_1.
DR SMART: SM00076; IFabd_1.
DR PROSITE: PS00252; INTERFERON_A_B_D_1.
KW pregnancy; Cytokine; Hormone; Antiviral; Signal; Glycoprotein.
FT CHAIN 1 23 BY SIMILARITY.
FT INTERFERON_TAU.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 195 AA; 22370 MW; 39599512F3C34208 CRC64;

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Query Match 6.5%; Score 80; DB 1; Length 195;
Best Local Similarity 27.4%; Pred. No. 3.5;
Matches 34; Conservative 17; Mismatches 33; Indels 40; Gaps 7;

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QY 13 SLLLLLLSPCLNGTPCYFSPHSP---ISSNFKV--KREITDHL----- 52
DB 6 SLLMALVAVSCPGSGSLCYLSRRPTLDVRENLRLLDMNRLSHSCQDQKQFGLPQEM 65
QY 53 -----LKDYPVTV-----AVNLQDEKCKRLNSFLAQKRIEOLKTVASKMOGLLE 100
DB 66 VEGDQLQDQDQALSVLYEMLQGRFNLFTHEHSCAMNTTL-----LEQLRT--GLHQQ--LE 117
QY 101 DYNF 104
DB 118 DLDLT 121

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RESULT 13
YVAG_SCHPO STANDARD; PRT; 1101 AA.
ID YVAG_SCHPO
AC 009733;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 126.5 kDa protein C31A2.16 in chromosome I.
GN SPAC31A2.16.

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OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DB).
CC
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CC
CC
DR EMBL: Z50113; CAA90474.1;
DR InterPro: IPR000219; RhGEF.
DR Pfam: PF00621; RhGEF; 1.
DR SMART: SM00325; RhGEF; 1.
DR PROSITE: PS00741; DH_1; FALSE_NEG.
DR PROSITE: PS50010; DH_2; 1.
KM Hypothetical protein.
FT DOMAIN 230
SQ SEQUENCE 1101 AA; 126537 MW; B26C47589F76F50B CRC64;

Query Match 6.5%; Score 79; DB 1; Length 1101;
Best Local Similarity 20.0%; Pred. No. 30;
Matches 42; Conservative 32; Mismatches 66; Indels 70; Gaps 8;

OY 37 PISNKKYKRELTDLHLD-----YPTVANVQDEKHCAL---WSFLAQRW 83
DB 815 PLSKEKEIGDELIDNLTETNEELLSHYPPNI-IVATFOKYLSSFNKRGVLLSSSF 873
OY 84 IEOLKTVAAGSKMOTLEDVN---TEIHFTVSCTFOPPLPECLRPVOTNISHLAKDTQTQ 138
DB 874 IQQLNRY-----ENLNLSFSTDAVYHKLTIQDLPESSKLLENIFSIASD--- 920
OY 139 LALKKCIGKACQNSRCLEVOCCPS-----STLPPRSP 175
DB 921 -LLRLPLADQCFVTKQIALALAPSMEGSNAVELYYLAYSRSRIGFTVEELPTPVSPA 979
OY 176 -----ALEATELPEPRROL 191
DB 980 NSNNKQIDSKFQALAMKEMPERHPKXIL 1009

RESULT 14
ID YW2_MYCTU STANDARD; PRT; 122 AA.
AC 050691;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical 12.9 kDa protein RV2272.
GN RV2272 OR MT2333 OR MTCY339-38C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
OC Actinomycetales; Corynebacteriales; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigemeier K., Gass S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,

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RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RT Nature 393:537-544 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M., Hat D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weisman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SUPPLEMENTARY LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO E.COLI YIDH.
CC
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CC
CC
DR EMBL: Z77163; CAB00963.1;
DR EMBL: AE007076; AAK46616.1;
DR TIGR: MT2333;
DR Tuberculist; RV2272;
DR InterPro: IPR003807; DUF202.
DR Pfam: PF02656; DUF202; 1.
KM Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 33 53
FT TRANSMEM 58 78
FT TRANSMEM 97 117
FT SEQUENCE 122 AA; 12994 MW; 23A5375426487A7 CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 122;
Best Local Similarity 33.0%; Pred. No. 2.8;
Matches 29; Conservative 12; Mismatches 24; Indels 23; Gaps 5;

OY 162 QPD-SSTLPPRSPALTEAT-----ELPEPRPRLDLLLPLTVLL 204
DB 13 EPDYRETTLANERTFLAWQRTALGILAAVALYQVLPETLTIGARQVGLVLA---LAIL 69
OY 205 AAAMG-LRWQARRRGELHPVPLRSH 231
DB 70 TSGMGLRWQADRAWRRH--LPLPRHP 95

RESULT 15
ID RCQ4_HUMAN STANDARD; PRT; 1208 AA.
AC 094761;
DT 30-MAY-2000 (rel. 39, Created)
DT 30-MAY-2000 (rel. 39, Last sequence update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE ATP-dependent DNA helicase Q4 (RecQ protein-like 4).
GN RECQ4 OR RECQ4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=9909744; PubMed=9878247;
RA Kitao S., Ohtsugi I., Ichikawa K., Goto M., Furuichi Y., Shimamoto A.,

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RT "Cloning of two new human helicase genes of the RecQ family:
RT biological significance of multiple species in higher eukaryotes.";
RL Genomics 54:443-452(1998).
RV [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-20021764; PubMed-10552928;
RA Kihao S., Lindor N.M., Shilatori M., Furuchi Y., Shimamoto A.;
RT Rothmund-Thomson syndrome responsible gene, RECQL4: genomic structure
RT and products.";
RL Genomics 61:268-276(1999).
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- DISEASE: DEFECTS IN RECQL4 ARE A CAUSE OF ROTHMUND-THOMSON
CC SYNDROME (RSTS). A DISEASE CHARACTERIZED BY DERMATOLOGICAL FEATURES
CC SUCH AS ATROPHY, PIGMENTATION, AND TELANGIECTASIA AND FREQUENTLY
CC ACCOMPANIED BY JUVENILE CATARACT, SADDLE NOSE, CONGENITAL BONE
CC DEFECTS, DISTURBANCES OF HAIR GROWTH, AND HYPOGONADISM.
CC -1- SIMILARITY: BELONGS TO THE HELICASE FAMILY. RECQ SUBFAMILY.
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CC -----
CC EMBL; AB006532; BAA74453.1; -
CC EMBL; AB026546; BAA86899.1; -
CC MIM; 603780; -
CC MIM; 268400; -
CC DR InterPro; IPR001410; DEAD.
CC DR InterPro; IPR001650; Helicase_C.
CC DR InterPro; IPR001878; ZnF_CCHC.
CC DR Pfam; PF00270; DEAD.1.
CC DR Pfam; PF00271; Helicase_C.1.
CC DR SMART; SM00487; DEXDC; 1.
CC DR SMART; SM00490; HELIC_C.1.
CC DR SMART; SM00343; ZnF_C2HC.1.
CC KW Hydrolyase; Helicase; ATP-binding; Nuclear protein.
CC NP_BIND 509
CC NP_BIND 509 APP (POTENTIAL).
CC SITE 605 608 DEAD BOX.
CC FT SEQUENCE 1208 AA; 133076 MW; CB809A7765AB48A1 CRC64;
SQ
Query Match 6.4%; Score 78.5; DB 1; Length 1208;
Best Local Similarity 22.8%; Pred. No. 37;
Matches 66; Conservative 27; Mismatches 111; Indels 85; Gaps 13;
QY 9 SPNSLL-LLLLSPCLGTPCYTS--HSPIS--SNPKYKRELDHLKIDPV 59
DB 523 SPCLLVSPILSLMDQVSGLPKCAACIHSGMRKQRESVLDKIRAAOVHVLMTPE 582
QY 60 T-----VAVNLQDEKICKALMSLFLAQRILEOLKTV----- 90
DB 583 ALVAGAGLPAAQLPVAFACIDBAHCLSQSHNFRPYLRYCKVYLREMGVHCFGLTA 642
QY 91 -----AGSKKQTLLEDFNFEIHVYISCTROPLECLRRVQVINSHL---KDCITOLL 140
DB 643 TATRTATADVAOHVAABEPDLH-----GAP-----VTNL-HLSMSMDRDDQAL 689
QY 141 ALKPCIGACONFS-----RCLEVOCOPDSSSTLLPPRSPTALEAT 180
DB 690 TLLQ--GKRFQNLDSIIYICNRREDTERIALRLTCLHAAMWPGSGRAFKTAAAHAG 747
QY 181 ELPEPRPQLLLLLPLTFVLLAAMGLRMQRRARRGELHPGVPLS 229
DB 748 MCSRRR-RKVRRAFMQGLRVVATVAFMGDLRPVRAVHLGLP-PS 794

DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polypeptide [Contains: N-terminal protein (P1); Helper
DE component proteinase (EC 3.4.22.-) (HC-PRO); Protein P3; 6 kDa protein
DE 1 (6K1); Cytoplasmic inclusion protein (C1); 6 kDa protein 2 (6K2);
DE Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A) (NIA
DE (EC 3.4.22.44) (49 kDa PRO); Nuclear inclusion
DE protein B (NI-B) (NIB) (RNA-directed RNA polymerase) (EC 2.7.7.48);
DE Coat protein (CP)].
DE Pepper mottle virus (California isolate) (PepMV) (Pepmov C).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Polyviridae;
OC Polyvirut.
OX NCBI_TaxID=31737;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93033110; PubMed-1413501;
RA VANCE V.B., Moore D., Turpen T.H., Bracker A., Hollowell V.C.;
RT "The complete nucleotide sequence of pepper mottle virus genomic RNA:
RT comparison of the encoded polypeptide with those of other sequenced
RT polyviruses.";
RL Virology 191:19-30(1992).
CC -1- FUNCTION: HELPER COMPONENT-PROTEINASE IS REQUIRED FOR APHID
CC TRANSMISSION AND ALSO HAS PROTEOLYTIC ACTIVITY.
CC -1- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY. IT
CC MAY BE INVOLVED IN REPLICATION.
CC -1- FUNCTION: NUCLEAR INCLUSION PROTEIN A HAS PROTEOLYTIC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Hydrolyses glutamyl bonds, and activity is
CC further restricted by preferences for the amino acids in p6 - P1'
CC that vary with the species of polyvirus, e.g. Glu-Xaa-Xaa-Tyr-Xaa-
CC Gln+Ser or Gly) for the enzyme from tobacco etch virus. The
CC natural substrate is the viral polypeptide, but other proteins and
CC oligopeptides containing the appropriate consensus sequence are
CC also cleaved.
CC -1- PIM: VPG IS COVALENTLY LINKED TO THE GENOMIC RNA.
CC -1- THE VIRAL RNA OF POTYVIRUSES IS EXPRESSED AS A SINGLE
CC POLYPEPTIDE WHICH UNDERGOES POSTTRANSLATIONAL PROTEOLYTIC
CC PROCESSING RESULTING IN THE PRODUCTION OF AT LEAST EIGHT
CC INDIVIDUAL PROTEINS.
CC -1- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
CC -1- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
CC -1- SIMILARITY: BELONGS TO THE POTYVIRUSES POLYPEPTIDE FAMILY.
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CC -----
CC EMBL; M96425; AAA46903.1; -
CC PIR; A44062; A44062.
CC MEROPS; C04.001; -
CC MEROPS; C06.001; -
CC MEROPS; S30.001; -
CC DR InterPro; IPR001410; DEAD.
CC DR InterPro; IPR001650; Helicase_C.
CC DR InterPro; IPR001730; Peptidase_C4.
CC DR InterPro; IPR001456; Peptidase_C6.
CC DR InterPro; IPR001592; Poly_P1.
CC DR InterPro; IPR001205; RNA_POL_P3D.
CC DR InterPro; IPR001254; Trypsin.
CC Pfam; PF00270; DEAD.1.
CC Pfam; PF00271; Helicase_C.1.
CC Pfam; PF00863; Peptidase_C4.1.
CC Pfam; PF00863; Peptidase_C6.1.
CC Pfam; PF00767; Poly_coat.1.
CC Pfam; PF01577; Poly_P1.1.
CC Pfam; PF00680; RNA_dep_RNA_POL.1.
CC PRINTS; PR00966; NIAPOTYVASE.
CC SMART; SM00487; DEXDC; 1.

DR SMART; SM00490; HELIC; 1.
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 287 N-TERMINAL PROTEIN.
 FT CHAIN 288 743 HELPER COMPONENT PROTEINASE.
 FT CHAIN 744 744 PROTEIN P3.
 FT CHAIN 1157 1156 6 KDA PROTEIN 1.
 FT CHAIN 1157 1790 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1791 1842 6 KDA PROTEIN 2.
 FT CHAIN 1843 2276 GENOME-LINKED PROTEIN.
 FT CHAIN 2277 2795 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2796 3068 NUCLEAR INCLUSION PROTEIN B.
 FT BINDING 1906 COVALENT LINKAGE OF VIRAL RNA
 (BY SIMILARITY).
 FT NP BIND 1241 1248 ATP (POTENTIAL).
 FT SEQUENCE 3068 AA; 348651 MW; FD3458B837FDA7C2 CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 3068;
 Best Local Similarity 25.4%; Pred. No. 1.1e+02;
 Matches 31; Conservative 19; Mismatches 61; Indels 11; Gaps 5;
 Oy 37 PISNFKVKEPRLDHLK-DY-PYVAVNLODEK---HCKALMSFLAQRNLEOKTV 90
 1612 PLSPS-STPRASSDWITAGDYRRIGVRLDIPEDTRIRFKTRKFTNNMESVLRK 1670
 Oy 91 AGSKMOTLEDVTEHETHEFTVCTFQPLPECLRFVQTNISHLKDTCTQLLAKPCIGKAC 150
 1671 ASAFPPLRSSITKIALYVLTDLVAIPRLTAVES---LLEDERKROYQFSLIDNGC 1726
 Oy 151 ON 152
 Db 1727 SS 1728

RESULT 17
 CM35_HUMAN STANDARD; PRT; 224 AA.
 ID CM35_HUMAN
 AC 008708;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE CMR35 antigen precursor.
 GN CMR35.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92249405; PubMed=1349532;
 RA Jackson D.G., Hart D.N.J., Starling G., Bell J.I.;
 RT "Molecular cloning of a novel member of the immunoglobulin gene
 superfamily homologous to the polymeric immunoglobulin receptor.";
 RL Eur. J. Immunol. 22:1157-1163(1992).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1- TISSUE SPECIFICITY: PRESENT ON THE SURFACE OF MONOCYTES,
 CC NEUTROPHILS, A PROPORTION OF PERIPHERAL BLOOD T AND B LYMPHOCYTES
 CC AND LYMPHOCTIC CELL LINES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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 CC EMBL; X66171; CAA46948.1; -

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig-MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; Ig; 1.
 KW Antigen; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 224 CMR35 ANTIGEN.
 FT DOMAIN 21 183 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 205 204 POTENTIAL.
 FT DOMAIN 205 224 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 36 117 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 123 175 PRO-RICH.
 FT DOMAIN 43 110 POTENTIAL.
 FT DISULFID 57 65 POTENTIAL.
 FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 99 39 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 224 AA; 24830 MW; 60C8871BD84600D2 CRC64;

Query Match 6.4%; Score 78; DB 1; Length 224;
 Best Local Similarity 23.1%; Pred. No. 6.1;
 Matches 60; Conservative 27; Mismatches 89; Indels 84; Gaps 12;
 Oy 5 APAPNSLSLLLLLSLSECLGTPDCYFSHSPISNFKVKEPRLDHLKDYPTVA-- 62
 3 ARAMASMRSSALLLLLVPG-----YF---PLS-----HPMTVACP 34
 Oy 63 -----VNIODEHCKAL--W-----SLFLAQRNLEOKTVAGSKMOTLEDVTEHETHEFTV 109
 35 VGSLSVQCYKEHEHETHEFTVCTFQPLPECLRFVQTNISHLKDTCTQLLAKPCIGKAC 93
 Oy 110 TSCFPQPLPECLRFVQTNISHLKDTCTQLLAKPCIGKACONFSRCLEVO 160
 94 -TVTLENLTF-----EDAGTYMCGVDPFWLRDFHDEIVEVSVPAQTGA 139
 Oy 161 COPDSS-----TLPPRSIALTELEPPRP-----ROLILLILLPLFLVTL 204
 140 SSPQSMGTSGPPTKLPVTPSVTRKDPSPHPSLSNVNRFLLVILLPLLSML 199
 Oy 205 AAA-WGIRWQARRRNGELHP 223
 Db 200 GAVLWVNRPRQSSRSRQNP 219

RESULT 18
 STFB_MYCGE STANDARD; PRT; 806 AA.
 ID STFB_MYCGE
 AC P47437; Q49516;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phenylalanine-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
 DE tRNA ligase beta chain) (Phers).
 GN PHET OR MG195.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmales; Mycoplasma.
 OX NCBI_TaxID=2097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;
 RX MEDLINE=96026346; PubMed=7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Eult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fitchman J.L., Weidman J.F., Small K.V., Sandusky M., Furmann J.L.,
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.F., Dougherty B.A., Bolt K.F., Hu P.-C., Inculet T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 RT "The minimal gene complement of Mycoplasma genitalium.";
 RL Science 270:397-403(1995).
 RN [2]
 RP SEQUENCE OF 1-94 AND 682-798 FROM N.A.
 RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=94075230; Pubmed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchinson C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing";
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
CC dihydrophosphate + L-phenylalanyl-tRNA(Phe).
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (by
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
CC CHAIN FAMILY. SUBFAMILY 1.
CC -----
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CC -----
DR EMBL: U39699; AAC71413.1; -;
DR EMBL: U01711; AAB01024.1; -;
DR EMBL: U02173; AAD12455.1; -;
DR TIGR: MG195; -;
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
FT CONFLICT 81 NANNINPNINKF -> MLITLITLHISCL (IN
FT REF. 2).
SQ SEQUENCE 806 AA; 92132 MW; D2F2BA6E9A064478 CRC64;

Query Match 6.4%; Score 78; DB 1; Length 806;
Best Local Similarity 26.7%; Pred. No. 26;
Matches 44; Conservative 18; Mismatches 59; Indels 44; Gaps 8;

QY 36 SPISNFKVFEFRETDLK-----DYPYVAVNLODEKCKAL--WSEFLAQRTIQL 87
DB 550 NPVSQNSVVRKSLIDSLKLVKTNNNYK-NELVNIFEFSITKQNSSELAVALVEKL 608
QY 88 KYVAGSGMQTLLEDVNT-----EIHFVTSCTFQPLECLRFV-----Q 125
DB 609 FTTSFNMQSGINDYFMKGLAKLIVANLGF--SCDFEPLDSDYFVNNQSLKTIWENQ 666
QY 126 TNISHLKDPCTQLAL--KPCIGKACONPSRCLEVCQCPSSRL 168
DB 667 IGFGLIKESLNNYDLNNKPIY-----CLEINLDRMLSSL 702

RESULT 19
YN61_YEAST STANDARD; PRT; 908 AA.
AC P42839;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 102.5 kDa protein in KRE1-HXT14 intergenic region.
GN YNL321W OR N0339.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / FY1676;
RA MEDLINE=96076632; Pubmed=7502583;
RT Matfahi M., Nicaud J.-M., Levesque H., Gaillardin C.;
RT "Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV
RT identifies six known genes, a new member of the hexose transporter
RT family and ten new open reading frames";
RL Yeast 11:1077-1085(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO S.POMBE SPAC521.04C.

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CC -----
DR EMBL: Z46259; CA86376.1; -;
DR EMBL: Z71597; CA96252.1; -;
DR SGD: S0005265; YNL321W
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 245 265
FT TRANSMEM 409 429
FT TRANSMEM 495 515
FT TRANSMEM 531 551
FT TRANSMEM 561 581
FT TRANSMEM 588 608
FT TRANSMEM 627 647
FT TRANSMEM 677 707
FT TRANSMEM 747 767
FT TRANSMEM 784 804
FT TRANSMEM 817 837
FT TRANSMEM 852 872
FT TRANSMEM 886 906
SQ SEQUENCE 908 AA; 102498 MW; 180E0EC77DC111E CRC64;

Query Match 6.4%; Score 78; DB 1; Length 908;
Best Local Similarity 23.1%; Pred. No. 29;
Matches 43; Conservative 25; Mismatches 60; Indels 58; Gaps 10;

QY 6 PAMSPNSLLD--LALLSP-----CLRGT--PDCYFHSPISSNFKVFR 47
DB 624 PASAGVSALLIFSMIVAFVPTVLEYEYGVSVNCAQDANDRDTFSHPPL-----KEN 677
QY 48 ELTDLKDYVYAVNL-----QDEKCKALMSFLAQ----- 81
DB 678 RLFTHVLIQMSISCAIVLFCAYIIGLWFTLRHAKMQLIADPTSTAPQOQNSHDA 737
QY 82 -RWIEQLKTVAGSGMQTLLEDVNTIEHFVTSCT--TFQPLECL-LRFVQTNISHLKDTG 136
DB 738 PNW-SRKSSTCIILMSTLLVYAIIEI--LVSCVAVLEDPISLPKPLGLTIFALIPRTT 794
QY 137 TQLIAL 142
DB 795 EFLNAI 800

RESULT 20
HBZD_CANFA STANDARD; PRT; 266 AA.
AC P18470;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DCA class II histocompatibility antigen, DR-1 beta chain precursor.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9031610; Pubmed=2370085;
RA Sarmiento U.M., Storb R.;
RT "Nucleotide sequence of a dog DRB cDNA clone";
RL Immunogenetics 31:396-399(1990).
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CC -----
DR EMBL: M29611: AAA30874.1; -.
DR PIR: A45844; A45844.
DR HSSP: P13760; ZSEB.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR000353; MHC_II_beta.
DR Pfam: PF00969; Ig_1.
DR ProDom: PD000328; MHC_II_beta; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW MHC II: Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 266
FT FT DLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 30 124 DR-1 BETA CHAIN.
FT DOMAIN 125 227 EXTRACELLULAR BETA-1.
FT TRANSMEM 228 250 EXTRACELLULAR BETA-2.
FT DOMAIN 251 266 CYTOPLASMIC TAIL.
FT DISULFID 44 108 BY SIMILARITY.
FT DISULFID 146 202 BY SIMILARITY.
FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 266 AA; 30151 MW; 4E8297BBF1ACDD67 CRC64;

Query Match 6.38; Score 77.5; DB 1; Length 266;
Best Local Similarity 19.98; Pred. No. 8.2;
Matches 55; Conservative 52; Mismatches 92; Indels 77; Gaps 12;

QY 4 LAPAMSPSSLLILLILSP---CLRGNP-----DCYFHSPISSNPKYKRELTMD 51
Db 7 LGSGSM--TALMLILVLPFPANAKRTPPHLEFVAKSSECFY---NGTERAREVERYT 60
QY 52 HLKDY-----PYTVAVNLQDE-----KCKKALMSLFLA 80
Db 61 HNRREFVAFDSVGEFRAVTELRGPAVESNMWQKEILQERATVDYCRNNGYTESFTV 120
QY 81 QRWLEQLTVAGSKMQLLEVDNTEHFVTSCT---FQPLRECLREYQTN-----IS 129
Db 121 QRREPTVTVYPTKQTL-----QHNNLVCSVNGFYPGHIEVRWLRNGOEERAGVST 174
QY 130 HLK--DTCTQLALKPCIGKACONFSRCLEVOCPDSSTLLPSPRTALFATRLPVRP 167
Db 175 GLIRNGDWTFOILVMLEIVPQSGEYV-----CQVHPSL--TSPTVTEWRAQSDSAQ 225
QY 188 RQLLLLLLLPLTLVLLAAWGLRWQARRRGELAP 223
Db 226 SKMLSGIGGFVLGLFLAVGLFIFERNQKGSHGLP 261

RESULT 21
GBR2_RAT
ID GBR2_RAT STANDARD; PRT; 940 AA.
AC O88871: O9OMU2: 09JK36;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE gamma-aminobutylic acid type B receptor, subunit 2 precursor (GABA-B
receptor 2) (GABA-B-R2) (Gb2) (GABABR2).
GN GABBR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RX MEDLINE=99087320; Pubmed=9872315;
RA Jones K.A., Borowsky B., Tamm J.A., Craig D.A., Durkin M.M., Dai M.,

RA Yao W.-J., Johnson M., Gunwaldsen C.A., Huang L.-Y., Tang C., Shen Q.,
RA Salom J.A., Morse K., Laz T., Smith K.E., Nagaratnam D., Noble S.A.,
RA Branchek T.A., Gerald C.;
RT "GABA(B) receptors function as a heteromeric assembly of the subunits
KT GABA(B)1 and GABA(B)R2";
RL Nature 396:674-679(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex, and Cerebellum;
RX MEDLINE=99087322; Pubmed=9872317;
RA Kaupmann K., Maltsevsk B., Schuler V., Heid J., Froestl W., Beck P.,
RA Mosbacher J., Bischoff S., Kulik A., Shigemoto R., Karschin A.,
RA Beller B.;
RT "GABA-B receptor subtypes assemble into functional heteromeric
RT complexes";
RL Nature 396:683-687(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=20193514; Pubmed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RT "Distribution of the GABA(B) receptor subunit gb2 in rat CNS";
RL Brain Res. 860:41-52(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RN [5]
RP R1A-R2 INTERACTION, AND VARIANTS TYR-337 AND PRO-19 INS.
RC TISSUE=Hippocampus;
RX MEDLINE=99102694; Pubmed=9872744;
RA Kuner R., Koehr G., Gruenewald S., Eisenhardt G., Bach A.,
RA Kornau H.-C.;
RT "Role of heteromer formation in GABA-B Receptor function.";
RL Science 283:74-77(1999).
CC -I- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES
CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYAPTIC
CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC
CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
CC ANTIINDOLEPTICION.
CC -I- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
CC HAPPEN.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
CC PLASMA MEMBRANE.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN BRAIN CORTEX, HIPPOCAMPUS, MEDIAL
CC CEREBELLUM, THALAMUS AND CEREBELLUM. COEXPRESSION IS SEEN IN
CC CEREBELLUM.
CC -I- DEVELOPMENTAL STAGE: ABUNDANT IN BRAIN CORTEX AND CEREBELLUM
CC THROUGHOUT POSTNATAL DEVELOPMENT WHEREAS ITS EXPRESSION IN SPINAL
CC CORD GRADUALLY DECREASES.
CC -I- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
CC -I- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
CC GABA-B RECEPTOR SUBFAMILY.
CC -----
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CC	-----	
DR	EMBL; AF074482; AAD03335.1; -	
DR	EMBL; AF011316; CAN08592.1; -	
DR	EMBL; AF038793; AAC63596.1; -	
DR	EMBL; AF109405; AAD03338.1; -	
DR	Interpro: IPR001828; ANF_receptor.	
DR	Interpro: IPR000337; GPCR_Mgr.	
DR	Pfam: PF00003; 7tm_3; 1.	
DR	Pfam: PF01094; ANF_receptor; 2.	
DR	PRINTS: PRO0248; GPCRMRG.	
DR	PROSITE: PS00979; G_PROTEIN_RECPT_P3.1; FALSE NEG.	
DR	PROSITE: PS00980; G_PROTEIN_RECPT_P3.2; FALSE NEG.	
DR	PROSITE: PS00981; G_PROTEIN_RECPT_P3.3; FALSE NEG.	
DR	PROSITE: PS00259; G_PROTEIN_RECPT_P3.4; 1.	
KW	G-protein coupled receptor; Transmembrane; glycoprotein; signal;	
KW	Postsynaptic membrane; Collod coll.; Polymyxin.	
FT	CHAIN	1
FT	CHAIN	41
FT	DOMAIN	41
FT	TRANSMEM	483
FT	DOMAIN	504
FT	TRANSMEM	522
FT	DOMAIN	543
FT	TRANSMEM	551
FT	DOMAIN	572
FT	TRANSMEM	597
FT	DOMAIN	618
FT	TRANSMEM	654
FT	DOMAIN	675
FT	TRANSMEM	691
FT	DOMAIN	712
FT	TRANSMEM	720
FT	DOMAIN	741
FT	DOMAIN	780
FT	CARBOHYD	89
FT	CARBOHYD	297
FT	CARBOHYD	388
FT	CARBOHYD	403
FT	CARBOHYD	452
FT	VARIANT	19
FT	VARIANT	19
FT	VARIANT	19
FT	CONFLICT	337
FT	CONFLICT	343
Q	SEQUENCE	940 AA; 105751 MW; 77BB42D833C7505D CRC64;

	Query Match	6.3%	Score 77.5;	DB 1;	Length 940;	
	Best Local Similarity	41.0%;	Pred. No. 34;			
Matches	25;	Conservative	0;	Mismatches	19;	Gaps 3;
QY	171 PRSFIALEATELPEPRPQLLLLLLPLPTVLAAMAGLFMQRARRRGELHGPCVLPESH	230				
Dd	10 PRPP-----PPPPPARDLLPLTSLILMLAPGAWG--WTGRGADR-----PPSSS	52				
Qy	231 P 231					
Dd	53 P 53					
RESULT	22					
YB95_METH						
ID YB95_METH	STANDARD;	PRT; 222 AA.				
AC	O27263;					
DT	16-OCT-2001 (Rel. 40; Created)					
DT	16-OCT-2001 (Rel. 40; Last sequence update)					
DT	16-OCT-2001 (Rel. 40; Last annotation update)					
DE	Hypothetical protein MTH1195.					
GN	MTH1195.					
OS	Methanobacterium thermoautotrophicum.					
OC	Archaea; Euryarchaeota; Methanobacterales; Methanobacteriaceae;					

0X	Methanothermobacter.
0Y	NCBI_TaxId=145262;
1N	[1]
1P	SEQUENCE FROM N.A.
1R	STRAIN-DELTA H;
1X	MEDLINE=98037514; PubMed=93771463;
2A	Smith D. R., Doncette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
2B	Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
2C	Harrison D., Hoang L., Keagle P., Lumm W., Pochler B., Qiu D.,
2D	Spadafora R., Vicare K., Wang Y., Wierzbowski J., Gibson R.,
2E	McJannet N., Caruso A., Bush D., Sater H., Patweli D., Prabhakar S.,
2F	McDougal S., Shlmer G., Goyal A., Pietrowski S., Church G.M.,
2G	Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
2H	"Complete genome sequence of Methanobacterium thermoautotrophicum
2I	delhi: functional analysis and comparative genomics.";
2J	Bacteriol. 179:7135-7155(1997).
2K	-I- SIMILARITY: TO M.JANNASCHIT MJ1481.
2L	-----
2M	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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2P	CC use by non-profit institutions as long as its content is in no way
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2R	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
2S	CC or send an email to license@isb-sib.ch).
2T	CC -----
2U	DR EMBL: AE000887; AAB85684.1; -
2V	DR Hypothetical protein; Complete proteome.
2W	DR SEQUENCE 222 AA; 24863 MW; A2FADDB6657CEA94 CRC64;

```

Query Match: 6.3%; Score 76.5; DB 1; Length 222;
Best Local Similarity 24.8%; Pred. No. 8.1;
Matches 37; Conservative 21; Mismatches 50; Indels 41; Gaps 6;

OY 47 RELTDLKDYPTVAVNLQDEKHCKALMSFLAOR-WIEOLKTVAQSKMOTLL----- 99
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 78 READHLDLADFGLEKRODPSEKRIEBAAGKLLIYNSSVKLLTKVAGVEKQNTLVGAPL 137
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
OY 100 -----EVTNNEHFVTSCTFQPLPE-CLRFQTNISHLTKPTCYQLATLPCIGKACQNF 153
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 138 SYDDMRKINFT-----PESALRGIEKTEIHLRNDIERKLDALDELVL----- 179
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
OY 154 SRCLEVOCCPDSSFTLLPPRSPALATEL 182
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 180 -----VVGEPDKSTVL-----LAAAEEL 198
      11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 23
VS09_ROT51
ID VS09_ROT51 STANDARD; PRT; 326 AA.
AC P03533;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glycoprotein VP7 (Serotype-specific antigen) (Outer shell
DE Glycoprotein).
DE S9.
GN S9.
OS Simian 11 rotavirus (strain SA11-Both).
OS Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OC NCBI_TaxID=37137;
CX [1]
RN RP
RP SEQUENCE FROM N.A.
RX MEDLINE=63221547; PubMed=6304692;
RA Both G.W., Mattick U.S., Bellamy A.R.;
RA "Serotype-specific glycoprotein of simian 11 rotavirus: coding
RA assignment and gene sequence.";
RA Proc. Natl. Acad. Sci. U.S.A. 80:3091-3095(1983).
RN [2]
RN RP
RP SEQUENCE FROM N.A.
RX MEDLINE=64165100; PubMed=6323768;
RA Arias C.F., Lopez S., Bell J.R., Strauss J.H.;
RA "Primary structure of the neutralization antigen of simian rotavirus

```

RT SAl1 as deduced from cDNA sequence.";
RL J. Vitrol. 50:657-661(1984).
CC -1- FUNCTION: VP7 IS THE MAJOR NEUTRALISATION ANTIGEN.
CC -1- SUBCELLULAR LOCATION: Rough endoplasmic reticulum.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: V01190; CAA24510.1; -
DR EMBL: V01546; CAA24788.1; -
DR EMBL: K02028; AAA47307.1; -
DR PIR: A04135; VGXRLS.
DR InterPro: IPR001963; VP7.
DR Pfam: PF00434; VP7; 1.
KW Coat protein; Transmembrane; Glycoprotein.
FT TRANSMEM 33 48
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 16 16 I -> T (IN REF. 2).
FT CONFLICT 32 32 C -> F (IN REF. 2).
FT CONFLICT 37 37 L -> F (IN REF. 2).
FT CONFLICT 60 60 T -> A (IN REF. 2).
FT CONFLICT 75 75 T -> P (IN REF. 2).
FT CONFLICT 114 114 G -> E (IN REF. 2).
FT CONFLICT 219 219 A -> P (IN REF. 2).
FT CONFLICT 269 269 L -> H (IN REF. 1); CAA24788).
SQ SEQUENCE 326 AA; 37119 MW; C75549HDI2A0C31 CRC64;

Query Match 6.3%; Score 76.5; DB 1; Length 326;
Best Local Similarity 28.4%; Pred. No. 13;
Matches 23; Conservative 10; Mismatches 31; Indels 17; Gaps 2;

QY 14 LLLLLLSPCLR-----GTPDCYFHSPTSSNFKKFRRLDHLKDYPTVA 62
DB 37 LLEFIVLSPFRKQNGYINLPITGSMWDPAYANSTOEEF-----LTSTLCVYPTMA 90
QY 63 VNODEKHCKALMSLFLAQRW 83
DB 91 TEINDNSMKDTLSOLFLLTKGM 111

RESULT 24
ASAL_ENTFA STANDARD; PRT; 1296 AA.
AC P17953;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Aggregation substance precursor.
GN ASAL.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Plasmid PAD1.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 44-51.
RC STRAIN-DS16;
RX MEDLINE=91014689; PubMed=2120541;
RA Galli D., Lottspeich F., Wirth R.;
RT "Sequence analysis of Enterococcus faecalis aggregation substance
RT encoded by the sex pheromone plasmid PAD1.";
RL Mol. Microbiol. 4:895-904(1990).
CC -1- FUNCTION: AGGREGATION SUBSTANCE ALLOWS DONOR AND RECIPIENT STRAINS
CC TO FORM TIGHT AGGREGATES WHICH ALLOW THE NON-MOTILE BACTERIA TO
CC MAINTAIN PHYSICAL CONTACT OVER A PERIOD OF TIME SUFFICIENT TO
CC PERMIT CONJUGATIVE TRANSFER OF THE SEX PHEROMONE PLASMID FROM
CC DONOR TO RECIPIENT STRAINS.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall.
CC -1- SIMILARITY: NO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
CC IN THE REGION OF THE MEMBRANE ANCHOR.
CC
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CC
DR EMBL: X17214; CAA35083.1; -
DR PIR: S10223; HMSOLF.
DR InterPro: IPR001899; Gram_pos_anchor.
DR Pfam: PF00746; Gram_pos_anchor; 1.
DR PROSITE: PS00343; GRAM_POS_ANCHORING; 1.
KW Plasmid; Transmembrane; Cell wall; Signal.
FT SIGNAL 1 43
FT CHAIN 44 126
FT DOMAIN 44 126
FT TRANSMEM 1269 1269
FT DOMAIN 1290 1296
FT DOMAIN 1223 1260
FT DOMAIN 1261 1266
FT
SQ SEQUENCE 1296 AA; 142285 MW; 52123A13AD23E5B CRC64;

Query Match 6.3%; Score 76.5; DB 1; Length 1296;
Best Local Similarity 20.8%; Pred. No. 60;
Matches 41; Conservative 29; Mismatches 62; Indels 65; Gaps 9;

QY 38 ISSNFKKFRRLDHLKDYPTVAANLDEKHCALMSLFLAQRWIDQLTVAGSKMQT 97
DB 1149 ISKLEFTEFGQGVKKTASQAFIDANLKENKNVAHSMKAFG---VRI--AGDVIYNT 1203
QY 98 LLEDVNTLHIFVTSCTFQPLPECLRFVQTN--ISHLKDYPTQALLAPCGKACQNSFR 155
DB 1204 IESFNNE-----KIKTNFVTVTRPE-----KP----- 1226
QY 156 CLEVGQCPDSSLTLPFR-----SPIALE-----ATELPEPRROLLLLPLTLYL 203
DB 1227 ----QTPEKTVIVPPTPTPQAPVPELVERKASVPELPDTGEGQNVLLTVAGSLAAM 1282
QY 204 LAAAMGLRMQRARRRGE 220
DB 1283 GLAGLGF-----KRRKE 1294

RESULT 25
DMD_CHICK STANDARD; PRT; 3660 AA.
AC P11533;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Dystrophin.
GN DMD.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89098331; PubMed=3062582;
RA Lemaire C., Heilig R., Mandel J.L.;
RT "Nucleotide sequence of chicken dystrophin cDNA.";
RL Nucleic Acids Res. 16:11815-11815(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;

RX MEDLINE-89210800; PubMed-3072195;
RA Lemaire C., Heilig R., Mandel J.L.;
RT "The chicken dystrophin cDNA: striking conservation of the C-terminal
FT coding and 3' untranslated regions between man and chicken.";
RL EMBO J. 7:4157-4162(1988).
CC -!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYOSKELETON TO THE
CC PLASMA MEMBRANE.
CC -!- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY
CC ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIBRININ,
CC ABP-120, ABP-180, OR BETA-FODRIN).
CC -!- SIMILARITY: CONTAINS 2 CALPONTIN-HOMOLOGY (CH) DOMAINS.
CC -!- SIMILARITY: CONTAINS 22 SPECTRIN REPEATS.
CC -!- SIMILARITY: CONTAINS 1 ZN-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: X13369; CAA31746.1; -.
DR PIR: S02041; S02041.
DR HSSP: P46939; 1BHD.
DR InterPro: IPR001589; Actinin_act_bind.
DR InterPro: IPR001715; Calponin_hom.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR001202; WW.
DR InterPro: IPR002349; WW_domain.
DR InterPro: IPR000433; Znf_ZZ.
DR Pfam: PF00307; CH; 2.
DR Pfam: PF00435; spectrin; 22.
DR Pfam: PF00397; WW; 1.
DR Pfam: PF00569; Zz; 1.
DR PRINTS: PR00403; WMDOMAIN.
DR SMART: SM00033; CH; 2.
DR SMART: SM00150; SPEC; 21.
DR SMART: SM00456; WW; 1.
DR SMART: SM00291; Znf_ZZ; 1.
DR PROSITE: PS00019; ACTININ_1; 1.
DR PROSITE: PS00020; ACTININ_2; 1.
DR PROSITE: PS00021; CH; 2.
DR PROSITE: PS01159; WW_DOMAIN_1; 1.
DR PROSITE: PS00020; WW_DOMAIN_2; 1.
DR PROSITE: PS01357; ZF_ZZ_1; 2.
DR PROSITE: PS01357; ZF_ZZ_2; 1.
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
KW Repeat; Zinc-finger.
FT DOMAIN 1 244 ACTIN-BINDING.
FT DOMAIN 19 123 CH 1.
FT DOMAIN 138 241 CH 2.
FT REPEAT 341 449 SPECTRIN 1.
FT REPEAT 450 558 SPECTRIN 2.
FT REPEAT 561 669 SPECTRIN 3.
FT REPEAT 721 830 SPECTRIN 4.
FT REPEAT 832 936 SPECTRIN 5.
FT REPEAT 945 1047 SPECTRIN 6.
FT REPEAT 1050 1156 SPECTRIN 7.
FT REPEAT 1159 1265 SPECTRIN 8.
FT REPEAT 1266 1369 SPECTRIN 9.
FT REPEAT 1470 1570 SPECTRIN 10.
FT REPEAT 1573 1678 SPECTRIN 11.
FT REPEAT 1681 1782 SPECTRIN 12.
FT REPEAT 1879 1981 SPECTRIN 13.
FT REPEAT 2013 2103 SPECTRIN 14.
FT REPEAT 2106 2211 SPECTRIN 15.
FT REPEAT 2214 2321 SPECTRIN 16.
FT REPEAT 2472 2574 SPECTRIN 17.
FT REPEAT 2577 2683 SPECTRIN 18.
FT REPEAT 2686 2799 SPECTRIN 19.
FT REPEAT 2802 2904 SPECTRIN 20.

FT REPEAT 2906 2928 SPECTRIN 21.
FT REPEAT 2931 3037 SPECTRIN 22.
FT DOMAIN 3052 3085 WW.
FT ZN_FING 3304 3351 ZN-TYPE.
FT VARIANT 1171 1171 MISSING.
FT VARIANT 1869 1869 0 -> H.
FT VARIANT 1885 1885 K -> R.
SQ SEQUENCE 3660 AA; 422874 MW; 85493DAF6D5B6D4A CRC64;
Query Match 6.3%; Score 76.5; DB 1; Length 3660;
Best Local Similarity 24.6%; Pred. No. 1.9e+02;
Matches 52; Conservative 37; Mismatches 83; Indels 39; Gaps 12;
QY 31 CYRSHSPISNFKVKKRRELTDHLKDY--PYVAVNLODEKHCALMSLFLAQRWITQLK 88
DB 3337 CFPS-GRVAKGKMHNP-----WVEYCTPTTSGEDVD--FAVVLNKKFRTKRYFAKHP 3387
QY 89 TVAGSKMOTLEDVNTETIHFTVSCFQPLPECIAPVQTNISHLKDKTQLALKP--C 145
DB 3388 RMGYLPVQTVLEGDNNETP-VTLINFWPVDALAMENSGNSYINDSISPRESIDDEHL 3446
QY 146 IGKACQNFSCLEVCQPDSSSTLLPPRSP---TALERTPEPRPRQLLLLLPLTL 201
DB 3447 IQHYCQSLNQ-----ESPLSOPRSPAQITLISEERGE-----LERILLADLEEN 3492
QY 202 VILAAAGLRWQARRRGELHPGV-PLPSHP 231
DB 3493 RNLA---EYDLKQOHD-HKGLSPPLSP 3518

Search completed: August 6, 2002, 09:46:22
Job time: 403 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:45:49 ; Search time 47.12 Seconds

(without alignments)
848,086 Million cell updates/sec

Title: US-09-448-378-2
1223

Sequence: 1 MTVLAPAMSPNSLLLLLL.....MORARRGELHPVPLPSHP 231

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP rivirus: *
16: SP bacteriap: *
17: SP archaeap: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87.9	71.9	172	11 061104	061104 mus musculu
2	779.5	63.7	292	6 09GKE0	09gke0 bos taurus
3	774	63.3	294	6 09MZV0	09mzv0 canis fam11
4	761	62.2	291	6 09MZU9	09mzu9 felis silve
5	678.5	55.5	274	6 09GKD9	09gkd9 bos taurus
6	95.5	7.8	909	10 042484	042484 arabidopsis
7	94	7.7	355	4 09H655	09h655 homo sapien
8	93.5	7.6	510	6 09BGV6	09bgv6 macaca fasc
9	90.5	7.4	909	10 09ASPS	09asps arabidopsis
10	88.5	7.2	326	12 083443	083443 murine rota
11	88.5	7.2	326	12 083448	083448 murine rota
12	88	7.2	258	4 09H563	09h563 homo sapien
13	88	7.2	765	4 094824	094824 homo sapien
14	88	7.2	843	4 014584	014584 homo sapien
15	87.5	7.2	1254	5 09VFS1	09vfi1 drosophila
16	87.5	7.2	477	11 09CYB2	09cyb2 mus musculu

17	87.5	7.2	1231	10 09FKE2	09fke2 arabidopsis
18	87	7.1	1256	5 09VFS0	09vfi0 drosophila
19	86.5	7.1	2111	5 091802	091802 drosophila
20	86.5	7.1	4167	5 09GPN8	09gpn8 drosophila
21	86	7.0	962	5 096164	096164 plasmidium
22	85	7.0	181	5 017726	017726 caenorhabdi
23	85	7.0	1305	2 006521	006521 enterococcu
24	85	7.0	4513	10 09MBP8	09mbf8 chlamydomon
25	84.5	6.9	364	4 096AV5	096av5 homo sapien
26	84.5	6.9	939	16 09KQC8	09kqc8 vibrrio chol
27	84	6.9	330	5 09H4U7	09h4u7 caenorhabdi
28	83.5	6.8	588	8 09B6D1	09b6d1 yarrowia li
29	83	6.8	258	4 09UMT2	09umt2 homo sapien
30	83	6.8	267	5 09W2D7	09w2d7 drosophila
31	83	6.8	1059	5 09VNP5	09vnp5 drosophila
32	82.5	6.7	326	12 085032	085032 porcine rot
33	82.5	6.7	326	12 085034	085034 porcine rot
34	82.5	6.7	335	8 09ZY32	09zy32 orycteropus
35	82.5	6.7	379	8 09T799	09t799 tapirus ind
36	82.5	6.7	431	10 09SN38	09sn38 arabidopsis
37	82.5	6.7	809	11 09DBY4	09db4 mus musculu
38	82.5	6.7	1266	10 09XET3	09xet3 lycopersico
39	82	6.7	575	10 09L568	09l568 arabidopsis
40	81.5	6.7	659	4 09H9U7	09h9u7 homo sapien
41	81.5	6.7	1148	4 09H6M7	09h6m7 homo sapien
42	81.5	6.7	7201	5 09VMT8	09vmt8 drosophila
43	81	6.6	348	8 09SA24	09sa24 conger myrl
44	81	6.6	2721	4 09B283	09b283 homo sapien
45	81	6.6	2721	4 096190	096190 homo sapien
46	81	6.6	4131	5 019542	019542 caenorhabdi
47	80.5	6.6	326	12 056347	056347 murine rota
48	80.5	6.6	326	12 083441	083441 murine rota
49	80.5	6.6	395	11 09DBN0	09dbn0 mus musculu
50	80.5	6.6	395	11 091XF8	091xf8 mus musculu

ALIGNMENTS

RESULT 1
061104
ID 061104 PRELIMINARY; PRT; 172 AA.
AC 061104:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FLT3 LIGAND, T169 FORM.
GN FLT3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Mattson J., Tsai S., Luh J., Guimares M.J., Mattei M.G., Rosnet O.,
RA Birnbaum D., Hannum C.,
RT "flt3 ligand: expression, genomic organization, alternatively spliced
forms and processing."
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U44024; AAA93305.1; -
DR MGD; MGI:95560; FLT3L.
DR InterPro; IPR004213; flt3_lig.
DR Pfam; PF02947; flt3_lig; I.
SQ SEQUENCE 172 AA; 19465 MW; 04FOA010171E3384 CRC64;

Query Match 71.9%; Score 879; DB 11; Length 172;
Best Local Similarity 98.2%; Pred No. 1.1e+82;
Matches 165; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MTVLAPAMSPNSLLLLLLSPCLRGTPDCYFSPHSNFKFVKFRETDLHLKDPVT 60
|||||

Db 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCCYFSHSPSSNFKYKRELDHLLKDYPT 60
 QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 Db 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 168
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 168

RESULT 2

09GKE0 PRELIMINARY; PRT; 292 AA.
 AC 09GKE0
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE FLT3 LIGAND ISOFORM-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20570936; PubMed=11120823;
 RA Mwangi W., Brown W.C., Palmer G.H.;
 RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
 RT required for receptor binding and function using naturally occurring
 RT ligand isoforms."
 RL J. Immunol. 165:6966-6974(2000).
 DR EMBL; AF282985; AAF99322.1; -;
 DR InterPro; IPR004213; flt3_1ig.
 DR Pfam; PF02947; flt3_1ig.1;
 DR SEQUENCE 292 AA; 32390 MW; D68B9ED79221202D CRC64;

Query Match 63.7%; Score 779.5; DB 6; Length 292;
 Best Local Similarity 63.2%; Pred. No. 3.5e-72;
 Matches 165; Conservative 20; Mismatches 43; Indels 33; Gaps 5;

QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCCYFSHSPSSNFKYKRELDHLLKDYPT 60
 Db 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCCYFSHSPSSNFKYKRELDHLLKDYPT 60
 QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 Db 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 180
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 180
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 180
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 180
 QY 181 ELPEPR-PROLLILLPLTVLLAAAGL-RWQARRR----- 218
 Db 179 SLFGPSPILLILLILLVALLATAMWLCRMRRRRRTYRGGERRTLRRESSHLPA 238
 QY 219 -----GELHPGVLPSPH 231
 Db 239 DTESELGSSQLPEP-PFLGHP 258
 RESULT 3
 09MZU0 PRELIMINARY; PRT; 294 AA.
 AC 09MZU0
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE FLT3 LIGAND.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20358731; PubMed=10902925;
 RA Yang S., Sim G.K.;
 RT "Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain."
 RL DNA Seq. 11:163-166(2000).
 DR EMBL; AF155148; AAF87088.1; -;
 DR SEQUENCE 294 AA; 32394 MW; 6859917A3B74ABCD CRC64;

Query Match 63.3%; Score 774; DB 6; Length 294;
 Best Local Similarity 70.2%; Pred. No. 1.3e-71;
 Matches 158; Conservative 23; Mismatches 38; Indels 6; Gaps 4;

QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCCYFSHSPSSNFKYKRELDHLLKDYPT 60
 Db 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCCYFSHSPSSNFKYKRELDHLLKDYPT 60
 QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 Db 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 180
 Db 120 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 177
 QY 181 ELPEPR-PROLLILLPLTVLLAAAGL-RWQARRR----- 224
 Db 178 ALPAPAR--LILLILLPALLLMSTWCLMRRRRRRRSPRPG 220

RESULT 4

09MZU0 PRELIMINARY; PRT; 291 AA.
 AC 09MZU0
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE FLT3 LIGAND.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20358731; PubMed=10902925;
 RA Yang S., Sim G.K.;
 RT "Molecular cloning of canine and feline flt3 ligand reveals high
 RT degree of similarity to the human and mouse homologue but uniquely
 RT long cytoplasmic domain."
 RL DNA Seq. 11:163-166(2000).
 DR EMBL; AF155149; AAF87089.1; -;
 DR SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64;

Query Match 62.2%; Score 761; DB 6; Length 291;
 Best Local Similarity 71.1%; Pred. No. 2.8e-70;
 Matches 155; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

QY 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCCYFSHSPSSNFKYKRELDHLLKDYPT 60
 Db 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCCYFSHSPSSNFKYKRELDHLLKDYPT 59
 QY 61 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 120
 Db 60 VAVNLQDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFOPLPEC 119
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 180
 Db 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSTLPPRSPALAEAT 180

Db	120	LRFQGNISHLQDPSSEQAALKEPWT--NFNSGCLDQCPSPSPPLPPSPALAEAT	177
QY	181	ELPEPRROLILILILPLTIVLTLAAAGLEWQARRR	218
Db	178	ALFAPQ-APULILILPLVALILMSAANCLHWRRR	214
RESULT	5		
Q9GKRD9		PRELIMINARY; PRT; 274 AA.	
AC	Q9GKRD9		
DT	01-MAR-2001	(Tremblrel. 16, Created)	
DT	01-MAR-2001	(Tremblrel. 16, last sequence update)	
DT	01-DEC-2001	(Tremblrel. 19, last annotation update)	
DE	ERT3 LIGAND ISOFORM-2.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-20570936; PubMed-11120823;		
RT	Mwangi W., Brown W.C., Palmer G.H.;		
RT	"Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain		
RT	required for receptor binding and function using naturally occurring		
RT	ligand isoforms."		
RL	J. Immunol. 165:6966-6974(2000).		
DR	EMBL: AF282986; AAF99323.1; .		
DR	InterPro: IPR004213; flt3_119.		
DR	Pfam: PF02947; flt3_119; 1.		
SO	SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA98B CRC64;		
Query Match	55.5%; Score 678.5; DB 6; Length 274;		
Best Local Similarity	57.5%; Pred. No. 8,2e-62;		
Matches 150; Conservative 19; Mismatches 41; Indels 51; Gaps			
QY	1	MTVLAPEWSPNSLLILLLSPCIRGPPDCYFSHSNPSSNFKKFKELTDHLKDPYT	60
Db	1	MTVLAPEWSPNSLLILLLSPGADGPPDCFSRSPSSFFAIIKILSKYLLDPPYT	60
QY	61	VAVNLDEKHCRAIMSLFLAQRWIEQLTFVAGSKMOTLEDVNEIHFFVNSCTFQPLPEC	120
Db	61	VASNLDDKRCGAFWFLVLAQRMRRLKTVAGSEMERKLEEDVNEIHFFVNSCAEQ-----	115
QY	121	LRFVQNTISHLKDCOTOLALPKPCIGKACQNSFCVCCQPPSSLLPPSPSIIEAT	180
Db	116	-----DTHQQLALKPMT--THRFKSCLELCQCPSPPLLPSPSGALGAT	160
QY	181	ELPEPR-PROLILILPLTIVLTLAAAGL-RWQARR-----	218
Db	161	SLRPGSPPLILILILPLVALILMTATWCLCRWRRRRRTYRPGERRRLTPRESSHLPA	220
QY	219	-----GELHGPVLPSPH	231
Db	221	DTESELGGSQLPFG-PFLGHP	240
RESULT	6		
Q42484		PRELIMINARY; PRT; 909 AA.	
AC	Q42484		
DT	01-NOV-1996	(Tremblrel. 01, Created)	
DT	01-NOV-1996	(Tremblrel. 01, last sequence update)	
DT	01-DEC-2001	(Tremblrel. 19, last annotation update)	
DE	RPS2 (DISEASE RESISTANCE PROTEIN RPS2).		
GN	RPS2 OR F20H18.200 OR A74G26050.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsidae.		
NCBI_TaxID=3702;			

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RP SEQUENCE FROM N.A.
RN [1]
RC STRAIN-COL-0;
RX MEDLINE=94377978; PubMed=8091210;
RA Bent A.F., Kunkel B.N., Dahlbeck D., Brown K.L., Schmidt R.,
RT Giraudat J., Jeung Y., Staskawicz B.J.;
RA RPS2 of Arabidopsis thaliana: a leucine-rich repeat class of plant
RT disease resistance genes.*;
RL Science 265:1856-1860(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95007758; PubMed=7923358;
RA Mindinos M., Katagiri F., Yu G., Ausubel F.M.;
RT "The A. thaliana disease resistance gene RPS2 encodes a protein
RT containing a nucleotide-binding site and leucine-rich repeats.";
RL Cell 78:1089-1099(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Beyan M., Rose M., Hempel S., Entian K.-D., Hohenseil J., Mewes H.W.,
RL Meyer K.F.X., Scheller C.;
RX Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RX Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RX Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RX Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RX EMBL: U14158; AAA21874.1; -
DR EMBL: U12860; AAA50236.1; -
DR EMBL: A1049483; CAB39674.1; -
DR EMBL: A1161564; CAB79464.1; -
DR InterPro: IPR001687; ATP_GRP_A.
DR InterPro: IPR007087; Disease_testist.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00560; LRR; 4.
DR Pfam: PF00931; NB-ARC; 1.
DR PRINTS: PR00364; DISEASERISIT.
SQ SEQUENCE 909 AA; 104640 MW; D279B6E30E49D640 CRC64;

Query Match 7.8%; Score 95.5; DB 10; Length 909;
Best Local Similarity 22.8%; Pred No. 0.36; Mismatches 89; Indels 57; Gaps
Matches 55; Conservative 40;

QY 14 LLLILLISPCLRGPDYCFSSHSPISNFKYFRRLD-----HLKDYPTVVA----- 62
DB 535 LTTLMLOQNSLSKRIPTGFEMHPVLRYLDFSFTISITPLRSIKYLVLEHLSMSGTKIS 594
QY 63 -----VNIDDEHCKALMSLF-----AQRWIEQLTKV-----AGSKWQTLLEDPVT 104
DB 595 VLPDELGNLKKLHLDLORTFOELQITPRDALQWLSKLEVLNLYSYAGWELQSGEDEAE 654
QY 105 EINH-----VTSCTRPFLPECLRR--VQTNISHLKLDCTQTLALK-PCIGK 148
DB 655 ELGAGDALEYENITLTGQITVLSLETKITLFFEGALNKKITQHLHVEECNELLYNNDPSLTN 714
QY 149 ACONFSKCLEVOCOPDSSLPRPSIALAEATELPERPRRQQLLLLLLLPLTIVLAAAM 208
DB 715 HGRNLR--LSIKSCHDLEYLV--TPADFENDWLPs--LEVLTLSHINHLTV-----W 762
QY 209 G 209
DB 763 G 763

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ID	09H665			
ID	09H665	PRELIMINARY,	PRT;	355 AA.
AC	09H665;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CDNA: FLJ22573 FIS, CLONE HS102387.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=SMALL INTESTINE;			
RA	Watanabe K., Kumagai A., Itakura S., Yamazaki M., Ota T.,			
RA	Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,			
RA	Nakamura Y., Isoigai T., Sugano S.;			
RT	"NEED human cDNA sequencing project."			
RL	Submitted (Aug-2000) to the EMBL/GenBank/DBD databases.			
DBLINK	AK026222, BAB15400.1, to the EMBL/GenBank/DBD databases.			
SQ	SEQUENCE 355 AA; 37894 MW; 52C41A73E673623C CRC64;			

Query Match 7.7%; Score 94; DB 4; Length 355;
Best Local Similarity 20.6%; Pred. No. 0.18;
Matches 41; Conservative 15; Mismatches 59; Indels 84; Gaps 6;

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QY 116 PLE-----CLRVQVNIHSLKDKTOLALIKPC-----IGKAC-----QNESCL 157
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 18 PPEPASOYCYGRLEIYNPNPNKCCSSCLORFPGPCPDYERENGCLNDGDFVTPFRKCS 77
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 158 EVOCQPDSSSTLLPP-----1721-----
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 SGCCNPDGAEILCPCGGGAVITPAAGGGRTPMRCREBPVPAKHGCIPLGNGAPSSQE 137
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 172 -RSPIALELTLPPEPPPC-----LLLLLLPLTVLVLLAANGLMQRARRGE 220
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 RSSPASSIAMRPPEPPPOAMPNPLPLVVLTLTLAVIALLLFTLLMLHLCMPREKADPY 197
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 221 LHPGV-----PLPSH 230
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 PYRELVCQVPNTHTPSSSH 216
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT	ID	ORGANISM	PRELIMINARY	PROTEIN	510 AA.
098Gy6	098Gy6	098Gy6			
AC	098Gy6	098Gy6			
DT	01-JUN-2001	(TREMBLrel, 17, Created)			
DT	01-JUN-2001	(TREMBLrel, 17, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel, 19, Last annotation update)			
DE	HYPOPHYSEAL 56.5 KDA PROTEIN				
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				
OC	Cercopithecoinae; Macaca.				
OX	NCBI_Taxid=9541;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=FRONTAL LOBE LEFT;				
RA	Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.				
RA	Suzuki Y., Sugano S., Hashimoto K.;				
RT	*Isolation of full-length cDNA clones from macaque brain cDNA				
RL	libraries.*;				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDbj databases.				
DR	EMBL: AB055271, BAB21895.1; -.				
DR	InterPro: IPR001611; LRR.				
DR	InterPro: IPR003592; LRR_out.				
DR	InterPro: IPR003591; LRR_typ.				
DR	Pfam: PF00560; LRR: 6.				
DR	PRINTS: PR00019; LEUICHRPT.				
DR	SMART: SM00370; LRR: 4.				
DR	SMART: SM00369; LRR_typ: 6.				

KW Hypothetical protein.
SQ SEQUENCE 510 AA; 56496 MW; FF52698C2F9119E8 CRC64;

Query Match 7.6%; Score 93.5; DB 6; Length 510;
 Best Local Similarity 23.9%; Pred. No. 0.3;
 Matches 68; Conservative 34; Mismatches 105; Indels 77; Gaps 14;

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0Y 9 SPNSLLLLLLLSPLCRTRDP-----CYSHSISNKKVRFREIYDHL- 35
Db STNLSLFLNLTALSLSRNGIEVOEDALDGLTMRLLLEHNOISS-----SLDHPF 103
0Y 54 --LKDPVYVAV-----LODE--KHKALMSFLAORMIEOL--KTVAGSKMOTL--LE 100
Db 104 SKLHSLOVLAISNNKLPRLGSGWFRNTRGLTRQLDONOITNLTSSFGTNLSHLHLD 163
0Y 101 DVNNEIHFVYSCGPDIPECPCLREVOTN-----ISHLKD-----TCRQLL 140
Db 164 LSNMFISYIKDAFRLDQ--LQEVDSLNNRLAHMPVETPRQLQGLIHLSDKNQMSCTCDL 222
0Y 141 -----AKPGICAGACNSRCLENOCODDSTLLPSPSLAEAELEPEPRQLLTL- 193
Db 223 HPLARELKNYIKSSAHLNKLKDLQCPSTLAAVAAQSYLRLSETNOCPRKPNFTYVLD 282
0Y 194 -LLLP-----LTYVLLAAMGL-----RMQARRRGELH 222
Db 283 RSPLLPEQDVALTLTVGFGAAGVLCGLGVYFNKLDQOGANBH 326

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ID	Q9ASP5	PRELIMINARY	PRU	909 AA.
AC	Q9ASP5			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	DISEASE RESISTANCE PROTEIN RPS2.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eudicots II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_Taxid=3702;			
XM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21231631; PubMed=11333251;			
RA	Barerlee D., Zhang X., Bent A.F.;			
RT	"Hsp90-leucine-rich repeat domain can determine effective interaction			
RT	between RPS2 and other host factors in Arabidopsis RPS2-mediated			
RT	disease resistance."			
RL	Genetics 158:439-450(2001).			
DR	EMBL; AF368301; AAK38117.1; -			
DR	InterPro; IPR003593; AAA.			
DR	InterPro; IPR001687; ATP_GTP_A.			
DR	InterPro; IPR000767; Disease_resist.			
DR	InterPro; IPR001611; LRR.			
DR	InterPro; IPR003592; LRR_out.			
DR	InterPro; IPR002182; NB-ARC.			
DR	Pfam; PF00560; LRR; 4.			
DR	Pfam; PF00931; NB-ARC; 1.			
DR	PRINTS; PR00364; DISEASERST.			
DR	SMART; SM00382; AAA; 1.			
DR	SMART; SM00370; LRR; 4.			
KW	ATP-binding			
SO	SEQUENCE 909 AA; 104613 MW; F8350F8B1B409DFA CMC64;			

Query March 7.48; Score 90.5; DB 10; Length 909;
Best Local Similarity 22.88; Pred No. 1.2;
Matches 55; Conservative 36; Mismatches 91; Indels 57; Gaps 11.

QY 14 LLLLLLSPCLRSTPCTYSHPSPISNNKRYAFRELT-----HLKDYYVYA----- 62
DB 535 LTTLMLDOONSLAKTIPGFFMHPYRVLRVDLSFTSTLPISIKIVELHNLMSGTKIS 594


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RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mervulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Stien-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitslks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -i COFACTOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).
DR EMBL: AE003709: AAF55209.1: -.
DR FLYBASE: FBgn0038349: CG6045.
DR InterPro: IPR002888: 2Fe-2S_BD.
DR InterPro: IPR000564: 2Fe2S_ferredoxin.
DR InterPro: IPR000674: Aldxan_dh_C.
DR InterPro: IPR002346: dehydrog_molyb.
DR InterPro: IPR001041: Ferredoxin.
DR Pfam: PF01315: Ald_xan_dh_C2; 2.
DR Pfam: PF02738: Ald_xan_dh_C2; 1.
DR Pfam: PF00941: PAD_binding_5; 1.
DR Pfam: PF00111: fer2; 1.
DR Pfam: PF01799: fer2_2; 1.
DR PRODOM: PD186071: 2Fe-2S_BD; 1.
DR PROSITE: PS00197: 2FE2S_FERREDOXIN; 1.
KW Iron-sulfur.
SQ
SEQUENCE 1254 AA: 13786 MW: 4CC7F24F15D80851 CRC64;

Query Match 7.2%; Score 88; DB 5; Length 1254;
Best Local Similarity 22.0%; Pred. No. 3.1;
Matches 39; Conservative 23; Mismatches 53; Indels 62; Gaps 7;

QY 21 LSPCLNGTPDCYFSHPISNFE-----VKKRFRELTJ-----HLKDYP 58
DB 655 LQPSL---GDVFPSPPTSPSRYVPASKSKKIKRSEQPDKEVGICFPMGQIYFTMEPQ 711
QY 59 VIVAVVLQDEKCKALMSFLAQRWIEQLKYAGSKMGQTLLEDVNTETI----- 107
DB 712 TVVALPFEDEG-----LKIFSATQMDQTOSTIAHMLQVKKAKDQVOLVRRLGGGYGSKIT 765
QY 108 -----FVTSCTFQPLPECLRFVQTNISHLLKDTCTOLLAKPCIGK--ACQNFSRC 156
DB 766 RGNQVACASLVAVYKLNRPVRYQS-----LESMDNDGKRMACRSYKRC 810

RESULT 16
Q9CYB2 PRELIMINARY; PRT; 477 AA.
AC Q9CYB2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 5730557B1SRK.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=12185660; Pubmed=11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischman W., Gaasterland T., Gissi C., King B., Kochi H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli P., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Norone P., Ring B., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK017844: BAB30970.1: -.
DR HSSP: P42773: 11HB.
DR MGD: MGI:1917904: 5730557B1SRK.
DR InterPro: IPR002110: ANK.
DR SMART: SM00248: ANK_4.
DR PROSITE: PS00086: ANK_REPEAT; 1.
DR PROSITE: PS50297: ANK_REPEAT_REGION; 1.
KW ANK repeat; Repeat.
SQ
SEQUENCE 477 AA: 52119 MW: 95A4ACF3891B967B CRC64;

Query Match 7.2%; Score 87.5; DB 11; Length 477;
Best Local Similarity 20.1%; Pred. No. 1.2;
Matches 47; Conservative 22; Mismatches 82; Indels 83; Gaps 8;

QY 19 LILSPCLNGTPDCYFSHPISNFEVKKRFRELTJDLKDYPYVAVNLQDEKCKALMSLF 78
DB 233 LMERPCPEQFGDKYKLEPL-----PAEAVLKSSGSKNCQIQRITAF 273
QY 79 LAQRWIEQLKYAGSKMGQTLLEDVNTETIHY--TSCFQPLPECLRFVQTNISHLLKDTIC 136
DB 274 LR-----STLTSRSQSGSLDEGVDLHVMYMTSLYSPA-----VAVVCCQYVC 316
QY 137 FOLLALPKPCIGKACQNFRCIL-----EVOCQDSDSLT-----PPRSP 174
DB 317 PE---NPEVCGRRRLAVQEIILAAQGNLNAQKDSNKKVDCSPQQLIFTRASSRSKSP 373
QY 175 ILLEATELEPPRRQLLLLLPLTLVLLAAMGLRMQRRARRRGELHPGVPLD 228
DB 374 AASRSTPAPVTRKASILPLQLL-----RRSSVAPGVVYP 407

RESULT 17
Q9FKE2 PRELIMINARY; PRT; 1231 AA.
AC Q9FKE2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DISEASE RESISTANCE PROTEIN RPS4.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=96403884; Pubmed=9734815;
RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
RA Tabata S.,
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
RT Sequence features of the regions of 1,367,185 bp covered by 19
RT physically assigned P1 and PAC clones."

```


NCBI_TaxID=7227;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed-10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amentides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Abriil J.F., Abdayani A.A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson A.,
 RA Merkulov G., Mielshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,
 RA Switzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao C., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003219; AAG22465.1; -
 DR FBASE: FBgn0001313; K1-2.
 DR InterPro: IPR001901; SecE.
 DR PROSITE: PS01067; SECE_SPE61G; UNKNOWN_1.
 SQ SEQUENCE 2111 AA; 242787 MW; 00DZA0DB87A3D36B CRC64;

Query Match 7.1%; Score 86.5; DB 5; Length 2111;
 Best Local Similarity 21.1%; Pred. No. 8.1;
 Matches 58; Conservative 42; Mismatches 90; Indels 85; Gaps 10;

QY 11 NSULLLLLLLSPCLGTPDCYFSH-----SPISNFYKFR----- 47
 DB 989 NGVLLTTEALYSFILLNVBD--FLHVALCFSPIGENFNSYROYAPALLSSTTPMFRFWP 1046
 QY 48 -----ELTDHLKDYEVTVAVN-LODEKHKAL--WSFLAQRWTEOLKTVAGSKMOTLL 99
 DB 1047 QEALLEVASHFLGFLPLNVVSGKEDEKRESLYVSTEAILQRODAYVFSYHSSVAKMS 1106
 QY 100 EDVNTET--HFVTS-----CTROPLEPCRFVQTNISHLKPTCQOLALK----- 143
 DB 1107 ENMYAEVKRYNYTSPNYIQLVSGFKLLKRRLEVSANRLNGLSKISFTQEKVSIM 1166
 QY 144 -----PCIGKACNFSRCLEVOQCQPSSTLLPSPRIAEATELPEPRROILL 192
 DB 1167 SEELKASSEQVKILARECEDFISMIEIQ-----KSEATEQKEKYDAEAVL 1211
 QY 193 LLLPLPTLVLLAAAGLQRARRRGELHPGVL 227
 DB 1212 IRDEITICLELAATA-----RADLEVMPM 1236

RESULT 20
 ID 096PN8 PRELIMINARY; PRT; 4167 AA.
 AC 096PN8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 GN 1-BETA DYNEIN (FRAGMENT).
 GN KL-2 OR CG17866.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridae; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20542110; PubMed-11069293;
 RA Carvalho A.B., Lazaro B.P., Clark A.G.;
 RT "Chromosomal fertility factors Kl-2 and Kl-3 of *Drosophila*
 RT melanogaster encode dynein heavy chain polypeptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13239-13244(2000).
 DR EMBL: AF313479; AAG29545.1; -
 DR FBASE: FBgn0001313; K1-2.
 DR InterPro: IPR003593; AAA.
 DR SMART: SM00382; AAA; 2.
 KW ATP-binding.
 FT NON_TER
 SQ SEQUENCE 4167 AA; 483035 MW; 5FA88C54B67CC205 CRC64;

Query Match 7.1%; Score 86.5; DB 5; Length 4167;
 Best Local Similarity 21.1%; Pred. No. 18;
 Matches 58; Conservative 42; Mismatches 90; Indels 85; Gaps 10;

QY 11 NSULLLLLLLSPCLGTPDCYFSH-----SPISNFYKFR----- 47
 DB 2592 NGVLLTTEALYSFILLNVBD--FLHVALCFSPIGENFNSYROYAPALLSSTTPMFRFWP 2649
 QY 48 -----ELTDHLKDYEVTVAVN-LODEKHKAL--WSFLAQRWTEOLKTVAGSKMOTLL 99
 DB 2650 QEALLEVASHFLGFLPLNVVSGKEDEKRESLYVSTEAILQRODAYVFSYHSSVAKMS 2709
 QY 100 EDVNTET--HFVTS-----CTROPLEPCRFVQTNISHLKPTCQOLALK----- 143
 DB 2710 ENMYAEVKRYNYTSPNYIQLVSGFKLLKRRLEVSANRLNGLSKISFTQEKVSIM 2769
 QY 144 -----PCIGKACNFSRCLEVOQCQPSSTLLPSPRIAEATELPEPRROILL 192
 DB 2770 SEELKASSEQVKILARECEDFISMIEIQ-----KSEATEQKEKYDAEAVL 2814
 QY 193 LLLPLPTLVLLAAAGLQRARRRGELHPGVL 227
 DB 2815 IRDEITICLELAATA-----RADLEVMPM 2839

RESULT 21
 ID 096164 PRELIMINARY; PRT; 962 AA.
 AC 096164;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE SERA ANTIGEN/PAPAIN-LIKE PROTEASE WITH ACTIVE SER.
 GN PFB0345C.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99021743; PubMed-9804551;
 RA Gardner M.J., Tetteelin H., Carucci D.J., Cummings L.M., Aravind L.,

RA Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
 RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
 RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
 RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
 RT falciparum";
 RL Science 282:1126-1132(1998).
 DR EMBL; AE001388; AAC71858.1; -.
 DR MEROPS; C01.UNA; -.
 DR InterPro: IPR000668; Peptidase-CL.
 DR InterPro: IPR000169; Thiolprol-actl_site.
 DR Pfam: PF00112; Peptidase-CL; 1.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
 DR HydroLase; Protease; Thiol protease.
 SQ SEQUENCE 962 AA; 108680 MW; BF7659CC46D39495 CRC64;

Query Match 7.0%; Score 86; DB 5; Length 962;
 Best Local Similarity 20.9%; Pred. No. 3.7;
 Matches 31; Conservative 28; Mismatches 39; Indels 50; Gaps 7;

QY 8 WSPNSLLILLLLSPCLKGTDPDYSHSPISNF-----KVFRELTDHL----- 53
 DB 422 WMNKKTGILL-----POLSYDLTYKNNNFTEFTQNSYTSQNIYDKLYCNHEXC 470
 QY 54 --LKDYPTVYA-VNLDEKHKALMSLFLAQRIEOLKTVAGSKMOTLLEDVNTFHEVT 110
 DB 471 NRIKDHNNICINVEDOKNCALSWA-FASKYHLETIKCMKG-----YEPINASVLYVT 523
 QY 111 SCTGFPLPECLRFVGTNISHLKDTCQTQ 138
 DB 524 NC-----LNKNKNDVCTE 536

RESULT 22
 017726 PRELIMINARY; PRT; 181 AA.
 AC 017726;
 DT 01-JUN-1998 (TrEMBLrel. 05, Created)
 DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE D1086.1 PROTEIN.
 GN D1086.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peleiderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RA Snye R.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RT none;
 RT "none sequence of the nematode C. elegans: A platform for
 RT investigating biology";
 RL Science 282:2012-2018(1998).
 RL EMBL; Z81491; CAB04019.1; -.
 DR InterPro: IPR002542; DUF19.
 DR Pfam: PF01579; DUF19; 1.
 SQ SEQUENCE 181 AA; 20198 MW; 80128F93F6A4E822 CRC64;

Query Match 7.0%; Score 85; DB 5; Length 181;
 Best Local Similarity 23.5%; Pred. NO. 0.69;
 Matches 39; Conservative 24; Mismatches 59; Indels 44; Gaps 8;

QY 13 SLLILLLLSPCLKGTDPDYSHSPISNFKVFRELTDHLKD-----PPTVAVNLQD 67
 DB 8 TILPFLFLSKAENSPIDSCSKDIDQIVTCRPLAKLIDKKKPLNSGPFVETLN-KM 66
 QY 68 EKHCKALMSLFLAQRIEOLKTVAGSKMOTLLEDVNTFHEVTSC---TFQPLD----- 118

DB 67 SGYCK-----EAMSCVSPAKCAPATEKMS---KFAFMKXTIDFMGPGYAOCAA 111
 QY 119 -----ECLRFVGTNISHLKD-TCYQALLAKRCI-----GKAC 150
 DB 112 LTKASNDKTECVOWYFSDKSRMSTDQKCAOFKAKKOCIEKDFGKAC 157

RESULT 23
 006521 PRELIMINARY; PRT; 1305 AA.
 AC 006521;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE AGGREGATION SUBSTANCE.
 GN ASH701.
 OS Enterococcus faecium (Streptococcus faecium).
 OG Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1352;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R7;
 RX MEDLINE=96257186; PubMed=8675038;
 RA Heaton M.P., Discotto L.F., Pucci M.J., Handwerker S.;
 RT "Mobilization of vancomycin resistance by transposon-mediated fusion
 RT of a VanA plasmid with an Enterococcus faecium sex pheromone-response
 RT plasmid";
 RL Gene 171:9-17(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R7;
 RA Heaton M.P., Handwerker S.;
 RT "Aggregation substance gene from Enterococcus faecium R7 pHK701.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U91527; AAB58159.1; -.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000566; Lipocin_cyFABP.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00213; LIPOCALIN; UNKNOWN_1.
 KW Plasmid.
 SQ SEQUENCE 1305 AA; 142496 MW; CBC342350A6F8A1 CRC64;

Query Match 7.0%; Score 85; DB 2; Length 1305;
 Best Local Similarity 21.1%; Pred. NO. 6.7;
 Matches 43; Conservative 29; Mismatches 60; Indels 72; Gaps 9;

QY 38 ISSNFVKVFRELTDHLKDYPTVAVNLQDEKHKALMSLFLAQRIEOLKTVAGSKMOT 97
 DB 1151 ISKLTMTPEQGVAVITASQAFLDAMNLKENKHVHSMKAFIG---VERI--AAGNVTNT 1205
 QY 98 LLEDVNTFHEVTSCFPDLPCLRFVGTN--ISHLKDTCYQALLAKPCGKACQNSR 155
 DB 1206 IESEFNNEF-----IKNTVYHTPE-----RP----- 1228
 QY 156 CLEVCQPDSSSTLLP-----PRSPALE-----ATLPPRPRLILLLL 196
 DB 1229 ----QTPPEKTYIVSTPTAPKTPQVPAQVAPFLVEKASVPLPDTGEGNILLTVA 1284

RESULT 24
 09MBP8 PRELIMINARY; PRT; 4513 AA.
 ID 09MBP8;
 AC 09MBP8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE 1 BETA DYNEIN HEAVY CHAIN.
 GN DYC10.
 OS Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=21 GR;
 RX MEDLINE=20346958; PubMed=10888669;
 RA Bertone C.A., Myster S.H., Bower R., O'Toole E.T., Porter M.E.;
 RT "Insights into the structural organization of the 11 inner arm dynein
 RT from a domain analysis of the 1 beta dynein heavy chain."
 RL Mol. Biol. Cell 11:2297-2313(2000).
 DR EMBL; AJ242523; CAB99316.1;
 DR EMBL; AJ242524; CAB99316.1; JOINED.
 DR EMBL; AJ242525; CAB99316.1; JOINED.
 DR InterPro; IPR004273; Dynein_heavy.
 DR InterPro; IPR000005; HTHARC.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF03028; Dynein_heavy; 1.
 DR PROSITE; PS00041; HTH_ARC_FAMILY_1; UNKNOWN_1.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
 SQ SEQUENCE 4513 AA; 510655 MW; F2A3E10767FD6719 CRC64;

Query Match 7.0%; Score 85; DB 10; Length 4513;
 Best Local Similarity 24.1%; Pred. No. 28;

Matches 49; Conservative 29; Mismatches 71; Indels 54; Gaps 10;

OY 47 RELDHLKD-----YPTAVANLQDEKCKALMSFLAQRIEQLKTVAGSKMOTLLE 100
 Db 796 RSISELVLDVEKKIYQAEFANLOESHNAKIDRLVSA---VDEIRDIMAS-IHVEE 851
 OY 101 DVNTEHFVSCFQPLPECLREFVQTNISHLKDTQTLLAKPCIGACONFSRCLEVQ 160
 Db 852 QDSEEVQ-----REWVRFTQ-KVDRKLED-----ALRHVKKSKQELSRLL--- 891
 OY 161 CQPDSSTLPP--RSPIALFATELPEPRP-----RQLLLILLPLTLVLLA 205
 Db 892 -NGDNKTEVPFHVTVWLETRNRELVRTIQALFTINSVARNLLVLQSVPRV----- 945
 OY 206 AAWGLRWORARRGELHPGVPLP 228
 Db 946 ---ALQLTKQRDMEDAGLPLP 965

RESULT 25

ID Q96AY5 PRELIMINARY; PRT; 364 AA.

AC Q96AY5;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE HYPOHETICAL 40.2 KDA PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA, AND CHORIOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016451; AHH16451.1; -.
 KW Hypothetical protein.
 FT NO_TER 1
 SQ SEQUENCE 364 AA; 40210 MW; A3D54D967D67FD30 CRC64;

Query Match 6.9%; Score 84.5; DB 4; Length 364;

Best Local Similarity 21.9%; Pred. No. 1.7;
 Matches 49; Conservative 22; Mismatches 80; Indels 73; Gaps 10;

OY 40 SNPKVFRELTDHLKDYPVTVAVNLQDEKCKALMSFLAQRIEQLKTVAGSK----- 94
 Db 35 SDNKVYHRSFCEANKKPKPIRMCMIOCTH-----PLWVAEEMERCTYCGSSGYOLRT 89
 OY 95 ---MOTLEDVNTETIFV-----TSCTFQPLP-----ECLRFV--OTNISH 130
 Db 90 VRCLOPLDGTIRSVHSKXCMGDRPESRRCNRYPCPAQMKKTGPMSECSYTCGEETEVQ 149
 OY 131 LL-----KDTCTQLLAKPCIGKAC-----QNTSRCLFVQC 161
 Db 150 VLCRAGDHCDGKPPSVRACQLPCNDPCIGDKSIFQOMEVLARYCSIPGYKILCCESC 209
 OY 162 QPDSSTLPPRSPIALFATEL-----PEPRRQLLLILLPLP 198
 Db 210 SKRSSI-LPP--PYLLEAETHDVIYSNPSDLPRSLVMPSTLVP 250

Search completed: August 6, 2002, 09:45:52
 Job time: 408 sec

19-MAY-1994; 94EP-0303575.

XX 24-MAY-1993; 93US-0068394.
 PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX
 PA (IMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman SD;
 XX
 DR WPI: 1995-008071/02.
 DR N-PSDB; AA079076.
 XX
 PR Isolated ligands for flt 3 receptors - useful for treating
 PR anaemia, AIDS and various cancers
 XX
 PS Disclosure: Page 25-27; 33pp; English.
 XX
 CC cDNA encoding mouse flt3-ligand (flt3-L) was isolated from a
 CC cDNA library of T-cell line F7B-0.344 in CY-1/EBNA-1 cells
 CC using a slide autoradiography method. Flt3-L stimulates
 CC production of progenitor and stem cells, and can be used e.g.
 CC in gene therapy protocols.
 CC
 XX
 SQ Sequence 231 AA:

Query Match 100.0%; Score 1223; DB 16; Length 231;
 Best Local Similarity 100.0%; Pred. No. 4.3e-115;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLISPCLRGTPDCYFSHSPSSNFKVRFRETLHLKDYPT 60
 |||||||
 Db 1 mtvlapawspnslllllllspclrgtpdcyfsnpsnkvrfreltdhlkdypt 60
 QY 61 VAVNLDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLEDVNTETHEFVTSCTFQPLPEC 120
 |||||||
 Db 61 vavnldekhekalslflaqrwieqlktvagskmqtlledvntethtfvtscftqplpec 120
 QY 121 LRFVQTNISHLKRTCTQLALAKPCIGKACQNFSCLEVQCQPDSSSTLLPPRSPIALEAT 180
 |||||||
 Db 121 lrfvqtnishlkrctqlalapkpcigkacqnfscleevqcpdssstllpprspialeat 180
 QY 181 ELPEPRPROLILLILLPLTLVLLAAAGLRMORARRRGEIHPGVLPSPHP 231
 |||||||
 Db 181 elpeprprqllllllllpltlvllaaaglrwqarrrrgelhpgvlpshp 231

RESULT 2
 AAW67768
 ID AAW67768 standard; Protein; 231 AA.
 XX
 AC AAW67768;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Murine flt3-ligand.
 XX
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;
 KW tissue transplantation.
 XX
 OS Mus sp.
 XX
 PN WO9857655-A1.
 XX
 PD 23-DEC-1998.
 XX
 PF 12-JUN-1998; 98WO-US12085.
 XX
 PR 17-JUN-1997; 97US-0877421.

XX
 PA (IMV) IMMUNEX CORP.
 XX
 PI Abbott NM, Mowat AM, Viney JL;
 XX
 DR WPI: 1999-070422/06.
 DR N-PSDB; AAV81505.
 XX
 PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 XX
 PS Claim 1: Page 12; 25pp; English.
 XX
 CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerising amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents murine flt3-L.
 CC
 XX
 SQ Sequence 231 AA:

Query Match 100.0%; Score 1223; DB 20; Length 231;
 Best Local Similarity 100.0%; Pred. No. 4.3e-115;
 Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLISPCLRGTPDCYFSHSPSSNFKVRFRETLHLKDYPT 60
 |||||||
 Db 1 mtvlapawspnslllllllspclrgtpdcyfsnpsnkvrfreltdhlkdypt 60
 QY 61 VAVNLDEKHKALMSLFLAQRWIEQLKTVAGSKMOTLEDVNTETHEFVTSCTFQPLPEC 120
 |||||||
 Db 61 vavnldekhekalslflaqrwieqlktvagskmqtlledvntethtfvtscftqplpec 120
 QY 121 LRFVQTNISHLKRTCTQLALAKPCIGKACQNFSCLEVQCQPDSSSTLLPPRSPIALEAT 180
 |||||||
 Db 121 lrfvqtnishlkrctqlalapkpcigkacqnfscleevqcpdssstllpprspialeat 180
 QY 181 ELPEPRPROLILLILLPLTLVLLAAAGLRMORARRRGEIHPGVLPSPHP 231
 |||||||
 Db 181 elpeprprqllllllllpltlvllaaaglrwqarrrrgelhpgvlpshp 231

RESULT 3
 AAB20186
 ID AAB20186 standard; Protein; 231 AA.
 XX
 AC AAB20186;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Mouse Flt-3 ligand.
 XX
 KW Flt-3 ligand; fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 XX
 OS Mus musculus.
 XX
 FH Key
 FH Peptide 1..27
 FH Protein /Label- Signal_peptide 28..231
 FH /Label- Mature_protein

FT	Domain	28..188
FT	/label= Extracellular_domain	
FT	Domain	189..211
FT	/label= Transmembrane_domain	
FT	Domain	212..231
FT	/label= Cytoplasmic_domain	
PN	WO200109303-A2.	
XX		
PD	08-FEB-2001.	
XX		
PE	31-JUL-2000; 2000WO-US20679.	
XX		
PR	30-JUL-1999; 99US-0146170.	
XX		
PA	(VICA-) VICAL INC.	
PI	Hermanson GG;	
DR	WPI: 2001-123319/13.	
XX		
DR	N-PSDB; AAF30305.	
XX		
PT	Immunogenic compositions comprising Flt-3 ligand encoding	
PT	polynucleotides and one or more antigen, or cytokine encoding	
PT	polynucleotides, useful for suppressing tumour growth and for treating	
PT	autoimmune diseases (e.g. rheumatoid arthritis) -	
XX		
PS	Claim 2; Page 120; 149pp; English.	
XX		
CC	The present sequence is that of mouse Fms-like tyrosine kinase	
CC	(Flt-3 ligand). The invention is directed to enhancing the	
CC	immune response of a vertebrate to an antigen or a cytokine by	
CC	administering in vivo, into a tissue of a vertebrate, a Flt-3	
CC	ligand-encoding polynucleotide, and 1 or more antigen- or	
CC	cytokine-encoding polynucleotides. The Flt-3 ligand-encoding	
CC	polynucleotide may encode the present full-length murine Flt-3	
CC	ligand polypeptide, or amino acids 28-163, 1-163, 28-189 or 1-189	
CC	of the Flt-3 ligand. The polynucleotides are incorporated into	
CC	the cells of the vertebrate in vivo, and a prophylactically or	
CC	therapeutically effective amount of Flt-3 ligand and 1 or more	
CC	antigens or cytokines is produced in vivo. Pharmaceutical	
CC	compositions comprising the polynucleotides are useful for	
CC	suppressing tumour growth in a mammal. The tumour is melanoma,	
CC	glioma or lymphoma, particularly B-cell lymphoma. They can also	
CC	be used for the prophylactic and/or therapeutic treatment of:	
CC	(a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B	
CC	and C in humans), parasitic (e.g. malaria) and fungal infections;	
CC	(b) autoimmune diseases (e.g. rheumatoid arthritis and	
CC	osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.	
CC	Various other examples of these diseases are given in the	
CC	specification.	
XX		
XX		
Sequence	231 AA;	
QY	Query Match	100.0%; Score 1223; DB 22; Length 231;
	Best Local Similarity	100.0%; Pred. No. 4.3e-115;
	Matches 231; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1	MTVLAPAMSPNSLLILLILLSPCIRGRPDCCFFSSPISSNFKVFRFETDLKLDYPT 60
Db	1	mtvlapawpsnslilililispclirpdcyfcfsspsnfkvfrfretldhikdypt 60
QY	61	VAVNIDRKHCKALMSFLAORMIOLKTVGSKMOTLLEDVNTFTHFPTSCFQPLRPC 120
Db	61	vavniqdehckalvslflaqwiesqlltvgasxmqtlledvntelhtvtsctfplpcc 120
QY	121	LRFVQTNISHLKDNCTQDLALPKCIGKACQNFRCLEVOCCOPDSSTLLPRSPIALEAT 180
Db	121	lrfvgtlnishllkdcctqllalkpqlgkacqnfrclevgcqdscstllprspialeat 180
QY	161	ELPEPRPRLILLILLLPLTLVLAAMGLKQARRRRGECHPGVLPDSHP 231

```

Db      101 elpeprpqlllllllpltlvlaawglwgrarrgghpyqlpsnp 231
        RESULT      4
        ID    AAR6177 standard; Peptide; 232 AA.
xx      AAR6177
AC      AAR6177;
xx      10-AUG-1995 (first entry)
DE      Mouse Mot110/T118 Flt3 ligand peptide fragment.
xx      Flt3 ligand; tyrosine kinase receptor ligand.
KW      Homo sapiens.
OS      W09426891-A.
xx      PD
xx      24-NOV-1994.
PF      18-MAY-1994; 94MO-US05150.
xx      PR
xx      19-MAY-1993; 93US-0065231.
PR      07-JUL-1993; 93US-0089263.
PR      16-JUL-1993; 93US-0092549.
PR      13-AUG-1993; 93US-0106340.
PR      24-AUG-1993; 93US-0112391.
PR      19-NOV-1993; 93US-0155111.
PR      03-DEC-1993; 93US-0162413.
xx      PA
PA      (INRM ) INST NAT SANTE & RECH MEDICALE.
xx      PA      (SCHE ) SCHERING CORP.
PI      Birnbaum D, Culpepper JA, Hannum CH, Lee FD;
xx      DR      WPI; 1995-006787/01.
DR      N-PSDB; AAQ79464.
xx      PT
PT      New ligand for the Flt3 tyrosine kinase receptor - and related
xx      PT      nucleic acid, vectors, host cells and antibodies, useful for
xx      PT      treating abnormal cell physiology and proliferation, e.g. cancer,
xx      PT      also for diagnosis and drug screening
xx      PS      Claim 11: page 79-80; 90pp; English.
CC      A cDNA library from the human stromal cell line 29SV48, in
CC      CC      pMT185, was screened with an 800 bp fragment derived from
CC      CC      mouse clone T118. This fragment encompasses the coding region
CC      CC      conserved between two mouse clones, T118 and T110. Approx. 20
CC      CC      positive clones were selected and partially sequenced. Two
CC      CC      clones, S86 and S109, were found to be approx. 75% homologous
CC      CC      to the mouse clones over the first 163 AAs. Clone S86 continued
CC      CC      to show homology to T110 until the stop codon, although to a
CC      CC      lesser degree, for an overall homology of 66%. Clones T118 and
CC      CC      S109 do not show homology to each other or to the other clones
CC      CC      after mouse residue 163 (human residue 160). An additiona mouse
CC      CC      clone designated MB8 has a 29 AA insert at the junction between
CC      CC      the common and divergent portions of the mouse ligand.
xx      SS
SS      Sequence 232 AA:
Oy      Query Match          99.1%; Score 1212.5; DB 16; Length 232;
        Best Local Similarity 99.6%; Pred.No. 5e-114;
        Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1.
Oy      1 MTVLAPAMSNSSLILLLLLSPLCRGPDYCFSPISNSFKYKFPRLDHLTKPYT 60
        Db      1 mvtlapawsnnslilllllspclrgpdycfnsplsnfkxkfelcdhllykypvt 60
Oy      61 VAVNVLOEKCKALMSFLAQRNIDQLKTVAAGSKMOTLLEDVNTEIFHVTSTCTOPLPKC 120

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Db 61 vavnlqdekhnckalwslflaqrwleqllktvagskmgllledvntelhfvtscftqplpec 120
QY 121 LRFVQTNIHSLKDTCTQLLAKPCIGKACQNFSCLEVOQCPDSSSTLLPPRSPIALEAT 180
Db 121 lrfvqtnishllkdtctqlgllkpcigkacqnfsclevoqcpdssstllpprsplaleat 180
QY 181 ELPEPRPRQ-LLLLLLLPLFTVLVLAAMGLRMORARRRGELHGPVLPSPHP 231
Db 181 elpeprprqlllllllllllplftvlvllaawglrwqrrrrgelhpgvpplpsph 232

RESULT 5
AAB20189
ID AAB20189 standard; Protein: 232 AA.
XX
AC AAB20189;
XX
DT 14-MAY-2001 (first entry)
XX
DE Mouse Flt-3 ligand.
XX
KW Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KW lymphoma; autoimmune disease; infection; gene therapy.
XX
OS Mus musculus.
XX
FH Key
FH Peptide 1..27
FT /label= Signal_peptide
FT Protein 28..232
FT /label= Mature_protein
FT Domain 28..188
FT /label= Extracellular_domain
FT Domain 189..212
FT /label= Transmembrane_domain
FT Domain 213..232
FT /label= Cytoplasmic_domain
XX
PN WO200109303-A2.
XX
PD 08-FEB-2001.
XX
PF 31-JUL-2000; 2000WO-US20679.
XX
PR 30-JUL-1999; 99US-0146170.
XX
PA (VIC-) VICAL INC.
XX
P1 Hermanson GG;
XX
DR WPI; 2001-123319/13.
DR N-PSDB; AAF30307.
XX
PT Immunogenic compositions comprising Flt-3 ligand encoding
PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -
XX
PS Claim 2; Page 125-126; 149pp; English.
XX
CC The present sequence is that of mouse Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present sequence of the mature
CC polypeptide. The polynucleotides are incorporated into
CC the cells of the vertebrate in vivo, and a prophylactically or
CC therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for

CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.
XX
SQ Sequence 232 AA:
XX
Query Match 98.8%; Score 1208.5; DB 22; Length 232;
Best Local Similarity 99.1%; Pred. No. 1.3e-113;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 MVLAPAMSPNSLLLLLLLSPCLRGIPDCYFSHPSSNFKVKFRELTHLKDHYVT 60
Db 1 mtvlapawspnslllllllllspclrgipdcyfsnpsnfkvfkrelthllkdypt 60
QY 61 VAVNLQDEKHCKALWSLFLAQRWLEQLKTVAGSKMGTLLLEDVNTLHFVTSCTFQPLPEC 120
Db 61 vavnlqdekhnckalwslflaqrwleqllktvagskmgllledvntelhfvtscftqplpec 120
QY 121 LRFVQTNIHSLKDTCTQLLAKPCIGKACQNFSCLEVOQCPDSSSTLLPPRSPIALEAT 180
Db 121 lrfvqtnishllkdtctqlgllkpcigkacqnfsclevoqcpdssstllpprsplaleat 180
QY 181 ELPEPRPRQ-LLLLLLLPLFTVLVLAAMGLRMORARRRGELHGPVLPSPHP 231
Db 181 elpeprprqlllllllllplftvlvllaawglrwqrrrrgelhpgvpplpsph 232

RESULT 6
AAU02129
ID AAU02129 standard; Protein: 288 AA.
XX
AC AAU02129;
XX
DT 29-AUG-2001 (first entry)
XX
DE Flt-3 ligand (FL) used to make chimeric immunogenic polypeptide.
XX
KW Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;
KW chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A;
KW ETA dII; antigenic; immunogenic; cytotoxic T cell response; tumour;
KW vaccine; immunotherapy.
XX
OS unidentified.
XX
PN WO200129233-A2.
XX
PD 26-APR-2001.
XX
PF 20-OCT-2000; 2000WO-US41422.
XX
PR 20-OCT-1999; 99US-0421608.
PR 09-FEB-2000; 2000US-0501097.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Wu T, Hung C;
XX
DR WPI; 2001-290921/30.
XX
PT New chimeric polypeptide, useful as anti-tumour vaccines, comprises
PT carboxy terminal fragment of heat shock protein, Flt-3 ligand or
PT cytoplasmic translocation domain of Pseudomonas exotoxin A and
PT antigenic polypeptide -
XX
PS Claim 9; Fig 19; 110pp; English.
XX

CC The sequence represents the amino acid sequence of Flt-3 ligand (FL)
 CC used in construction of a chimeric polypeptide comprising: (a) a first
 CC polypeptide domain containing a carboxy terminal fragment of a heat shock
 CC protein (HSP), an Flt-3 ligand (FL), a cytoplasmic translocation domain
 CC of a Pseudomonas exotoxin A (ETA dII), or a granulocyte-macrophage colony
 CC stimulating factor (GM-CSF); and (b) a second polypeptide domain
 CC containing an antigenic polypeptide. A composition comprising the
 CC chimeric polypeptide is useful for inducing an immune response such as a
 CC cytotoxic T cell response. The nucleic acid or vector encoding the
 CC chimeric polypeptide present in the composition is administered as naked
 CC DNA by gene gun or equivalent, or by liposomal formulation. These are
 CC thus useful for vaccinating a mammal against infection by inducing an
 CC immune response to a pathogen. Preferably they are useful for vaccinating
 CC a mammal against a tumour antigen. The compositions and methods are
 CC useful for stimulating or enhancing the immunogenicity of a selected
 CC antigen or stimulating or enhancing a cellular immune response specific
 CC for that antigen. The chimeric nucleic acid molecules and vaccination
 CC methods, yield potent antigen-specific immunotherapy. The polynucleotides
 CC and DNA vaccines can induce a cellular immune response that is at least
 CC 40 fold more potent than conventional DNA vaccines. The vaccines are safe
 CC and useful for administration to domesticated or agricultural animals, as
 CC well as humans, and have low immunogenicity.

CC Sequence 288 AA;

Query Match 82.3%; Score 1006; DB 22; Length 288;
 Best Local Similarity 99.5%; Pred. No. 4.4e-93;
 Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISNFKVRFRELDHLKDPYT 60
 Db 1 mtylapawspnslllllllllspclrgtpdcyfspsnsfkvrfreltdhllkdyprt 60
 QY 61 VAVNLODEKHCKALMSLFLAQRWIEQLKTAVGSKMOTLLEVDNVEIHFWISCTFQPLPEC 120
 Db 61 vavnldexhckalmslflaqrwieqlktvagskmtllledvnteihfwtscftqplpec 120
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCDPDSSTLLPPRSPIALEAT 180
 Db 121 lrfvqtnishllkdtctqlalpkpcigkacqnfsrclevoqcdpsstllpprsialeat 180
 QY 181 ELPEPRPRQ 190
 Db 181 elpeprprqm 190

RESULT 7
 AAB20187
 ID AAB20187 standard; Protein; 189 AA.
 XX

AC AAB20187;

DT 14-MAY-2001 (first entry)

XX Mouse Flt-3 ligand (secreted form).

XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.

OS Mus musculus.

XX Location/Qualifiers

FT Peptide

FT 1..27 /label= Signal_peptide

FT 28..189 /label= Mature_protein

XX MO200109303-A2.

XX 08-FEB-2001.

XX PD

PF 31-JUL-2000; 2000WO-US20679.
 XX
 PR 30-JUL-1999; 99US-0146170.
 XX
 PA (VICA-) VICAL INC.
 XX
 PI Hermanson GG;
 XX
 DR WPI: 2001-123319/13.
 XX
 DR N-PSDB: AAF30305, AAF30313.
 XX
 PT Immunogenic compositions comprising Flt-3 ligand encoding
 PT polynucleotides and one or more antigen, or cytokine encoding
 PT polynucleotides, useful for suppressing tumour growth and for treating
 PT autoimmune diseases (e.g. rheumatoid arthritis) -

Claim 2; Page 121; 149pp; English.

CC The present sequence is that of a secreted form of mouse Fms-like
 CC tyrosine kinase (Flt-3 ligand), lacking the transmembrane and
 CC cytoplasmic domains of the full-length form (see AAB20186). This
 CC secreted form of the Flt-3 ligand is expressed by vector VR6200
 CC (see AAF30313). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, such as VR6200, and 1 or more
 CC antigen- or cytokine-encoding polynucleotides. The polynucleotides
 CC are incorporated into the cells of the vertebrate in vivo, and a
 CC prophylactically or therapeutically effective amount of Flt-3
 CC ligand and 1 or more antigens or cytokines is produced in vivo.
 CC Pharmaceutical compositions comprising the polynucleotides are
 CC useful for suppressing tumour growth in a mammal. The tumour is
 CC melanoma, glioma or lymphoma, particularly B-cell lymphoma. The
 CC co-injection of VR6200 and tumour-specific antigen-encoding plasmid
 CC VR1623 into mice significantly enhanced protection from tumour
 CC challenge. The claimed pharmaceutical compositions can also be
 CC used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.

CC Sequence 189 AA;

Query Match 82.1%; Score 1004; DB 22; Length 189;
 Best Local Similarity 100.0%; Pred. No. 4e-93;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISNFKVRFRELDHLKDPYT 60
 Db 1 mtylapawspnslllllllllspclrgtpdcyfspsnsfkvrfreltdhllkdyprt 60
 QY 61 VAVNLODEKHCKALMSLFLAQRWIEQLKTAVGSKMOTLLEVDNVEIHFWISCTFQPLPEC 120
 Db 61 vavnldexhckalmslflaqrwieqlktvagskmtllledvnteihfwtscftqplpec 120
 QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCDPDSSTLLPPRSPIALEAT 180
 Db 121 lrfvqtnishllkdtctqlalpkpcigkacqnfsrclevoqcdpsstllpprsialeat 180

QY 181 ELPEPRPRQ 189

Db 181 elpeprprqm 189

RESULT 8

AAB20191

ID AAB20191 standard; Protein; 172 AA.

XX

AC AAB20191;

XX 14-MAY-2001 (first entry)
 DT Mouse Flt-3 ligand.
 DE
 XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /label= Signal_peptide
 FT 28..172
 FT Protein /label= Mature_protein
 XX
 XX WO200109303-A2.
 XX 08-FEB-2001.
 XX 31-JUL-2000; 2000WO-US20679.
 XX 30-JUL-1999; 99US-0146170.
 XX (VICA-) VICAL INC.
 XX
 XX Hermanson GG;
 XX WPI; 2001-123319/13.
 DR N-PSDB; AAF30309.
 XX
 PT Immunogenic compositions comprising Flt-3 ligand encoding
 PT polynucleotide and one or more antigen, or cytokine encoding
 PT autoimmune diseases (e.g. rheumatoid arthritis) -
 XX
 PS Claim 2; Page 130; 149pp; English.
 XX
 CC The present sequence is that of mouse Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen- or
 CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
 CC polynucleotide may encode the present sequence or the mature
 CC polypeptide. The polynucleotides are incorporated into
 CC the cells of the vertebrate in vivo, and a prophylactically or
 CC therapeutically effective amount of Flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.
 CC
 XX
 XX Sequence 172 AA;
 SQ
 Query Match 71.9%; Score 879; DB 22; Length 172;
 Best Local Similarity 98.2%; Pred. No. 1.4e-80;
 Matches 165; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 61 vavnlqdekhckalwslflaqrwleqllktvagskmqtlledvnteihfvtsctfpdlpec 120
 QY 121 LRFVQNTNISHLKQCTQLLAKPICIGKACQNFSCLEVCQOPDSSRL 168
 DB 121 lrfvqntnshllkctcqlalkpcigkacqnfsclewcqpdarvsl 168
 RESULT 9
 AAB20188
 ID AAB20188 standard; Protein; 220 AA.
 XX
 XX AAB20188;
 AC
 XX
 XX 14-MAY-2001 (first entry)
 DT
 XX
 DE Mouse Flt-3 ligand.
 XX
 XX Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
 KW immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT /label= Signal_peptide
 FT 28..220
 FT Protein /label= Mature_protein
 XX
 XX WO200109303-A2.
 XX 08-FEB-2001.
 XX 31-JUL-2000; 2000WO-US20679.
 XX 30-JUL-1999; 99US-0146170.
 XX (VICA-) VICAL INC.
 XX
 XX Hermanson GG;
 XX WPI; 2001-123319/13.
 DR N-PSDB; AAF30306.
 XX
 PT Immunogenic compositions comprising Flt-3 ligand encoding
 PT polynucleotide and one or more antigen, or cytokine encoding
 PT autoimmune diseases (e.g. Rheumatoid arthritis) -
 XX
 PS Claim 2; Page 123-124; 149pp; English.
 XX
 CC The present sequence is that of mouse Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen- or
 CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
 CC polynucleotide may encode the present sequence or the mature
 CC polypeptide. The polynucleotides are incorporated into
 CC the cells of the vertebrate in vivo, and a prophylactically or
 CC therapeutically effective amount of Flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.

```

XX      XX      Sequence      220 AA;
SQ      Query Match
          71.9%; Score 879; DB 22; Length 220;
          Best Local Similarity 82.3%; Pred. No. 2e-80;
          Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY      1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISNFYKFKRELTDHLKDYPT 60
          1 mcvlapawspnslllllllspclrgtpdcyfsishpsisnfkfkreltdhllkdyprt 60
          Db
          61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLEDVNTIEHVTSCFQPLPEC 120
          61 vavnlqdekhckalmslflaqrmieqlktvagskmtlledvntiehvtscfqpplpec 120
          Db
          121 LRFVQTNISHLKDCCTQLALKPCIGKACQNFSCLEVOCPDSSITLPPRS----PIA 176
          121 lrfvqtnishllkdcctqalalkpcigkacqnfsrclevgcqpgng---gpraqhngatr 177
          Db
          177 LEATELPEPRRQDLLL-----LILLPLTLVLAA 206
          178 ltatalltvcpglllpivgtshmfllpyflsflls 212

RESULT 10
AAB20190
ID      AAB20190 standard; Protein; 220 AA.
XX
AC      AAB20190;
XX
DT      14-MAY-2001 (first entry)
XX
DE      Mouse Flt-3 ligand.
XX
KW      Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
KW      immunotherapy; therapy; tumour; cancer; melanoma; glioma;
KW      lymphoma; autoimmune disease; infection; gene therapy.
OS      Mus musculus.
XX
FH      Key
FT      Peptide      1..27      Location/Qualifiers
FT      Protein      /label= Signal_peptide
FT      Protein      /label= Mature_protein
XX
PN      WO200109303-A2.
XX
PD      08-FEB-2001.
XX
PF      31-JUL-2000; 2000WO-US20679.
XX
PR      30-JUL-1999; 99US-0146170.
XX
PA      (VICA-) VICAL INC.
XX
PI      Hermanson GG;
XX
DR      WPI; 2001-123319/13.
DR      N-PSDB; AAF30308.
XX
PT      Immunogenic compositions comprising Flt-3 ligand encoding
PT      polynucleotide and one or more antigen, or cytokine encoding
PT      polynucleotides, useful for suppressing tumour growth and for treating
PT      autoimmune diseases (e.g. rheumatoid arthritis) -
XX
PS      Claim 2; Page 128; 149pp; English.
XX
CC      The present sequence is that of mouse Fms-like tyrosine kinase
CC      (Flt-3 ligand). The invention is directed to enhancing the
CC      immune response of a vertebrate to an antigen or a cytokine by
CC      administering in vivo, into a tissue of a vertebrate, a Flt-3

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CC      ligand-encoding polynucleotide, and 1 or more antigen- or
CC      cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC      polynucleotide may encode the present sequence or the mature
CC      polypeptide. The polynucleotides are incorporated into
CC      the cells of the vertebrate in vivo, and a prophylactically or
CC      therapeutically effective amount of Flt-3 ligand and 1 or more
CC      antigens or cytokines is produced in vivo. Pharmaceutical
CC      compositions comprising the polynucleotides are useful for
CC      suppressing tumour growth in a mammal. The tumour is melanoma,
CC      glioma or lymphoma, particularly B-cell lymphoma. They can also
CC      be used for the prophylactic and/or therapeutic treatment of:
CC      (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC      and C in humans), parasitic (e.g. malaria) and fungal infections;
CC      (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC      osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC      Various other examples of these diseases are given in the
CC      specification.
XX
SQ      Sequence      220 AA;

Query Match
          71.9%; Score 879; DB 22; Length 220;
          Best Local Similarity 82.3%; Pred. No. 2e-80;
          Matches 177; Conservative 5; Mismatches 21; Indels 12; Gaps 3;

QY      1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISNFYKFKRELTDHLKDYPT 60
          1 mcvlapawspnslllllllspclrgtpdcyfsishpsisnfkfkreltdhllkdyprt 60
          Db
          61 VAVNLQDEKHCALMSLFLAQRMIEQLKTVAGSKMOTLEDVNTIEHVTSCFQPLPEC 120
          61 vavnlqdekhckalmslflaqrmieqlktvagskmtlledvntiehvtscfqpplpec 120
          Db
          121 LRFVQTNISHLKDCCTQLALKPCIGKACQNFSCLEVOCPDSSITLPPRS----PIA 176
          121 lrfvqtnishllkdcctqalalkpcigkacqnfsrclevgcqpgng---gpraqhngatr 177
          Db
          177 LEATELPEPRRQDLLL-----LILLPLTLVLAA 206
          178 ltatalltvcpglllpivgtshmfllpyflsflls 212

RESULT 11
AAV58204
ID      AAV58204 standard; Protein; 294 AA.
XX
AC      AAV58204;
XX
DT      14-MAR-2000 (first entry)
XX
DE      Canine Flt-3 ligand.
XX
KW      Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;
KW      immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS      Canis familiaris.
XX
PN      WO9961618-A2.
XX
PD      02-DEC-1999.
XX
PF      28-MAY-1999; 99WO-US11942.
XX
PR      29-MAY-1998; 98US-0087306.
XX
PA      (HESK-) HESKA CORP.
XX
PI      Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR      WPI; 2000-072623/06.
DR      N-PSDB; AA255487, AA255488, AA255489, AA255490.
XX
PT      Nucleic acids encoding immunoregulatory proteins from cats or dogs,

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Key	Location/Qualifiers
Peptide	1..26
Protein	/label= Signal_peptide
Domain	27..235
Domain	/label= Mature_protein
Domain	27..182
Domain	/label= Extracellular_domain
Domain	183..205
Domain	/label= Transmembrane_domain
Domain	206..235
Domain	/label= Cytoplasmic_domain

WO200109303-A2.
 08-FEB-2001.
 31-JUL-2000; 2000WO-US20679.
 30-JUL-1999; 99US-0146170.
 (VICIA-) VICAL INC.
 Hermonson GC;
 WPI; 2001-123319/13.
 N-PSDB; AAF30312.
 Immunogenic compositions comprising Flt-3 ligand encoding polynucleotide and one or more antigen, or cytokine encoding polynucleotide, useful for suppressing tumor growth and for treating autoimmune diseases (e.g. rheumatoid arthritis) -
 Claim 2; Page 137-138; 149pp; English.
 The present sequence is that of human Fms-like tyrosine kinase (Flt-3 ligand). The invention is directed to enhancing the immune response of a vertebrate to an antigen or a cytokine by administering in vivo, into a tissue of a vertebrate, a Flt-3 ligand-encoding polynucleotide, and 1 or more antigen- or cytokine-encoding polynucleotides. The Flt-3 ligand-encoding polynucleotide may encode the present full-length human Flt-3 ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235 of the Flt-3 ligand. The polynucleotides are incorporated into the cells of the vertebrate in vivo, and a prophylactically or therapeutically effective amount of Flt-3 ligand and 1 or more antigens or cytokines is produced in vivo. Pharmaceutical compositions comprising the polynucleotides are useful for suppressing tumor growth in a mammal. The tumor is melanoma, glioma or lymphoma, particularly B-cell lymphoma. They can also be used for the prophylactic and/or therapeutic treatment of: (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B and C in humans), parasitic (e.g. malaria) and fungal infections; (b) autoimmune diseases (e.g. rheumatoid arthritis and osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs. Various other examples of these diseases are given in the specification.

Sequence 235 AA:
 50

[illegible]

Sequence	235 AA
14	AA67541
15	AA67541 standard; Protein; 235 AA.
16	AA67541;
17	05-AUG-1995 (first entry)
18	Human flt-3 ligand.
19	flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.
20	Homo sapiens.
21	Location/Qualifiers
22	1..26
23	/label= Sig_peptide
24	/note= "signal peptide may extend to position 27"
25	27..182
26	/label= Extracellular_domain
27	/note= "extracellular domain may start at position 28"
28	183..205
29	/label= "transmembrane_domain
30	206..235
31	/label= Cytoplasmic_domain
32	EP627487-A.
33	07-DEC-1994.
34	19-MAY-1994; 94EP-0303575.
35	24-MAY-1993; 93US-0068394.
36	12-AUG-1993; 93US-0106463.
37	25-AUG-1993; 93US-0111758.
38	03-DEC-1993; 93US-0162407.
39	07-MAR-1994; 94US-0209502.
40	11-MAY-1994; 94US-0243545.
41	(IMV) IMMUNEX CORP.
42	Beckmann MP, Lyman SD;
43	WPI: 1995-008071/02.
44	N-PSDB; AA079079.
45	Isolated ligands for flt 3 receptors - useful for treating
46	anaemia, AIDS and various cancers
47	Disclosure; Page 29-30; 33pp; English.
48	A human T-cell lambda-gli10 random primed cDNA library was
49	screened with a fragment corresponding to the extracellular
50	domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AA079076)
51	to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
52	stem cells, and can be used e.g. in gene therapy protocols.

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Query Match      63.2%  Score 772.5  DB 22  Length 235;
Best Local Similarity 70.7%  Pred. No. 1.2e-69;
Matches 164;  Conservative 17;  Mismatches 42;  Indels 9;  Gaps
OY  1  MTVALPAMPSPNSLLLLLLSPCLRGTPDCYVSHSPDISNFKVYKREITDHLKDPVPT 60
Db  1  mtvlapawsp-ty:|||||||s|sgfsgdscfghspisdfeavrkirelsdy||qdy|pvt 59
OY  61  VAVNLDDEKCKKAKNSLFLAQRTEQKTKVAGSMQTLLEDVTEFHHPTVSCOTDPLDEC 120
Db  60  vaasldgeelcgaklwtlylaqqrmerlktvayagsmglleryntelhtvltkacqppsc 119

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Query Match	62.8%;	Score 768.5;	DB 16;	Length 235;
Best Local Similarity	70.3%;	Pred. No. 3e-69;		
Matches 163;	Conservative 17;	Mismatches 43;	Indels 9;	Gaps 4;

CC may be used to treat a pathological condition e.g. myelodysplasia,
CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
CC leukemia.

SO Sequence 235 AA:

Query Match 62.8%; Score 768.5; DB 21; Length 235;
Best Local Similarity 70.3%; Pred. No. 3e-69;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

OY 1 MYVLAPAMSPNSLLILLILLLSPCLRGTPDCYFSHPSPSSNFKYKFRRLDHLKDPVT 60
DB 1 mcvlapawsp-ctylllllllllssglsqgdcsfqhspsidfavkktlrsdyllqdyprt 59
OY 61 VAVNLODEHKCKALMSLPLAQRIEQLKTVAGSKMOTLLEDVNTIEHFVNSCTQPLPEC 120
DB 60 vasnlqdeecgllwrlvlaqgrwmerlktvagskmgllervnteihfvkcafqpppsc 119
OY 121 LRFVOTNISHLKDKCTQLALAKPCIGKACONFSRCLEVOCOPSSSTLLPPRSPIALEAT 180
DB 120 lrtvqunlsrlllqetseqvalkpwlttr--qnfsclelqcpdsscllppwsprrpleat 177
OY 181 ELPEPRPRLILLILLPLTFLVLAAMGLRWQRARRR---GELHPGVPLP 228
DB 178 aptapqpp--llllllllpyglllllaawclhmwqtrrrtrrrppgqgvppvpsp 227

RESULT 17

ID AAB20192 standard; Protein; 235 AA.

XX AAB20192;

DT 14-MAY-2001 (first entry)

XX Human Flt-3 ligand.

XX Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;

KW Immunotherapy; therapy; tumour; cancer; melanoma; glioma;

KW Lymphoma; autoimmune disease; infection; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..26 /Label- Signal_peptide

FT Protein 27..235 /Label- Mature_protein

FT Domain 27..182 /Label- Extracellular_domain

FT Domain 183..205 /Label- Transmembrane_domain

FT Domain 206..235 /Label- Cytoplasmic_domain

XX WO200109303-A2.

PD 08-FEB-2001.

PF 31-JUL-2000; 2000WO-US20679.

PR 30-JUL-1999; 99US-0146170.

PA (VICA-) VICAL INC.

PI Hermanson GG;

XX WPI, 2001-123319/13.

DR N-PSDB; AAF30310.

XX Immunogenic compositions comprising Flt-3 ligand encoding

PT polynucleotide and one or more antigen, or cytokine encoding
PT polynucleotides, useful for suppressing tumour growth and for treating
PT autoimmune diseases (e.g. rheumatoid arthritis) -

PS Claim 2; Page 132-133; 149pp; English.

CC The present sequence is that of human Fms-like tyrosine kinase
CC (Flt-3 ligand). The invention is directed to enhancing the
CC immune response of a vertebrate to an antigen or a cytokine by
CC administering in vivo, into a tissue of a vertebrate, a Flt-3
CC ligand-encoding polynucleotide, and 1 or more antigen- or
CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
CC polynucleotide may encode the present full-length human Flt-3
CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
CC or 27-235 of the ligand. The polynucleotides are incorporated
CC into the cells of the vertebrate in vivo, and a prophylactically
CC or therapeutically effective amount of Flt-3 ligand and 1 or more
CC antigens or cytokines is produced in vivo. Pharmaceutical
CC compositions comprising the polynucleotides are useful for
CC suppressing tumour growth in a mammal. The tumour is melanoma,
CC glioma or lymphoma, particularly B-cell lymphoma. They can also
CC be used for the prophylactic and/or therapeutic treatment of:
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
CC and C in humans), parasitic (e.g. malaria) and fungal infections;
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
CC Various other examples of these diseases are given in the
CC specification.

SO Sequence 235 AA:

Query Match 62.8%; Score 768.5; DB 22; Length 235;
Best Local Similarity 70.3%; Pred. No. 3e-69;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

OY 1 MYVLAPAMSPNSLLILLILLLSPCLRGTPDCYFSHPSPSSNFKYKFRRLDHLKDPVT 60
DB 1 mcvlapawsp-ctylllllllssglsqgdcsfqhspsidfavkktlrsdyllqdyprt 59
OY 61 VAVNLODEHKCKALMSLPLAQRIEQLKTVAGSKMOTLLEDVNTIEHFVNSCTQPLPEC 120
DB 60 vasnlqdeecgllwrlvlaqgrwmerlktvagskmgllervnteihfvkcafqpppsc 119
OY 121 LRFVOTNISHLKDKCTQLALAKPCIGKACONFSRCLEVOCOPSSSTLLPPRSPIALEAT 180
DB 120 lrtvqunlsrlllqetseqvalkpwlttr--qnfsclelqcpdsscllppwsprrpleat 177
OY 181 ELPEPRPRLILLILLPLTFLVLAAMGLRWQRARRR---GELHPGVPLP 228
DB 178 aptapqpp--llllllllpyglllllaawclhmwqtrrrtrrrppgqgvppvpsp 227

RESULT 18

ID AAY58210 standard; Protein; 291 AA.

XX AAY58210;

DT 14-MAR-2000 (first entry)

XX Feline Flt-3 ligand.

KW Flt-3 ligand; antibody; canine; feline; inhibitor; immune response;

KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.

OS Fells catus.

PN WO9961618-A2.

XX 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11942.

PR	29-MAY-1998:	980S-0087306.
XX	(HESK-) HESKA CORP.	
PA	Slim G., Yang S., Dreitz MJ., Wonderling RS,	
PL	WPI: 2000-072623/06.	
DR	N-PSDB: AA255518, AA255519, AA255520, AA255521.	
XX	Nucleic acids encoding immunoregulatory proteins from cats or dogs,	
PT	useful for treating or preventing e.g. tumors or autoimmune disease	-
XX	Claim 3c: Page 186-187; 264pp; English.	
XX	Sequences AAY58204 and AAY58206-Y58209 respectively represent	
CC	encoded, mature, clone 1 and clone 19 canine Flt-3 ligand, while	
CC	sequences AAY58210-Y58211 represent encoded and mature feline Flt-3	
CC	ligand. The invention relates to canine Interleukin-4 (IL-4),	
CC	canine or feline Flt-3 ligand, canine or feline CD40, canine or	
CC	feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline	
CC	interferon-alpha (IFN-alpha) and feline granulocyte macrophage	
CC	colony-stimulating factor (GM-CSF), and nucleotides which encode these	
CC	immunoregulatory proteins. The proteins, their associated	
CC	nucleic acids, specific antibodies and inhibitors may be used as	
CC	vaccines for therapeutic or prophylactic regulation of an immune	
CC	response in animals (particularly cats, dogs, horses and humans).	
CC	They may be used to treat autoimmune or infectious diseases including	
CC	allergies, tumours, inflammation and graft rejection, and to increase	
CC	the response from a co-administered antigen. The nucleotide sequences	
CC	can also be used for the recombinant production of a protein, while	
CC	nucleotide fragments are useful as probes, as amplification primers and	
CC	as sources of inhibitory therapeutics (e.g., antisense	
CC	oligonucleotides). The proteins may be used to raise antibodies and to	
CC	screen for modulators of activity, while the antibodies may be used in	
CC	detection, and in drug targeting.	
XX	Sequence 291 AA:	
SQ		
<hr/>		
Query Match	62.2%; Score 761; DB 21; Length 291;	
Best Local Similarity	71.1%; Pred. No. 2.2e-68;	
Matches 155; Conservative 22; Mismatches 37; Indels 4; Gaps		3
OY	1 MTVALPAPMSNSSLLILLILSLPCLRGTPDCYFSHPSPSSNNFKVFRLETFDHLKDVPYV 60	
Db	1 mivlaewsppts-111 59	
OY	61 VAVVLADEKCKAKALMSFLAQRIRIIDLKTIVAGSKQTLLLEDVNTGRIHFVNSCTFRQLPEC 120	
Db	60 vashlqgdclcgfwmhvlavlagrwmgglkavagsqmqsllaevnfeihvltcaigqbpjsc 119	
OY	121 LRFQVTINSHLKDTCFTOLATLKPCIGKACONFSRCLTVCOCOPSTLTLPSPFIALL 180	
Db	120 lrfqtgnishlqdtsegaalkpwtr--infsgclslqgpssaplprrpralcat 177	
OY	181 ELPEPRRRQLLLLLLLLPLETVLTLAAAWGLRMQRARR 218	
Db	178 alpepg-aplllllllllpvalllmsaaawlhwrttrwr 214	
<hr/>		
RESULT 19		
AAY69721		
ID	AAY69721 standard; Protein; 212 AA.	
XX	AAY69721:	
AC	05-JUL-2000 (first entry)	
XX	Human flt-3 mutein L-3H.	
DE		
XX	Immunomodulator; immunosuppressive; cytoskeletal; antianemic; anti-HIV;	
XX	neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;	

[illegible]

Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCYSHSPISSENVKRELTDLKDYPTAVANLQDEHCKALMSFLAQRWITQL 87
 Db 1 tqdcstqhspsissdflavkirelsdyllqdyptvasnldqdeicggllwrlvlagqrmerl 60

QY 88 KTVAGSKMOTLEDVNTETHEFTVSCFQPLPCELRFOVQTNISHLKDCQTQLALKPCIG 147
 Db 61 ktvagskmgqllervntelhfvtkcafgppscrlfvgtnisrlllgeseqvalkpwit 120

QY 148 KACQNFSCLEVCQCPDSSSTLLPRSPALAEATELPEPRPQQLLLPLTVLAAA 207
 Db 121 r--qntsrclqdcqdsstlppwsprrleatpqp--lllllllpvgllllaaa 176

QY 208 WGLRMQRRRR---GELHPGVLP 228
 Db 177 wclhwgrtrrrtprrpgeqyppvpssp 201

RESULT 22
 AAY69720
 ID AAY69720 standard; Protein; 209 AA.
 XX AC AAY69720;
 XX DF 05-JUL-2000 (first entry)
 XX DE Mature wild type human flt-3 protein.
 XX KM Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KM neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia.
 XX OS Homo sapiens.
 XX PN WO200001823-A2.
 XX PD 13-JAN-2000.
 XX PF 25-JUN-1999; 99WO-US14296.
 XX PR 02-JUL-1998; 98US-0109100.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Graddis TJ, McGrew JT;
 XX DR WPI: 2000-182115/16.
 XX DR N-PSDB; AA259064.
 XX PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX PS Claim 1; Page 89-90; 90pp; English.
 XX CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (this sequence) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,

CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 XX SQ Sequence 209 AA;

Query Match 56.1%; Score 686; Db 21; Length 209;
 Best Local Similarity 69.8%; Pred. No. 5.3e-61;
 Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCYSHSPISSENVKRELTDLKDYPTAVANLQDEHCKALMSFLAQRWITQL 87
 Db 1 tqdcstqhspsissdflavkirelsdyllqdyptvasnldqdeicggllwrlvlagqrmerl 60

QY 88 KTVAGSKMOTLEDVNTETHEFTVSCFQPLPCELRFOVQTNISHLKDCQTQLALKPCIG 147
 Db 61 ktvagskmgqllervntelhfvtkcafgppscrlfvgtnisrlllgeseqvalkpwit 120

QY 148 KACQNFSCLEVCQCPDSSSTLLPRSPALAEATELPEPRPQQLLLPLTVLAAA 207
 Db 121 r--qntsrclqdcqdsstlppwsprrleatpqp--lllllllpvgllllaaa 176

QY 208 WGLRMQRRRR---GELHPGVLP 228
 Db 177 wclhwgrtrrrtprrpgeqyppvpssp 201

RESULT 23
 AAY69723
 ID AAY69723 standard; Protein; 209 AA.
 XX AC AAY69723;
 XX DF 05-JUL-2000 (first entry)
 XX DE Human flt-3 mutain K84E.
 XX KM Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KM neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia; mutain.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200001823-A2.
 XX PD 13-JAN-2000.
 XX PF 25-JUN-1999; 99WO-US14296.
 XX PR 02-JUL-1998; 98US-0109100.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Graddis TJ, McGrew JT;
 XX DR WPI: 2000-182115/16.
 XX PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 XX PS Claim 4; Page 84-85; 90pp; English.
 XX CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3

CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 CC
 XX Sequence 209 AA;

Query Match 56.1%; Score 686; DB 21; Length 209;
 Best Local Similarity 69.8%; Pred. No. 5.3e-61;
 Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 28 TPDCYSHSPISSENFVKRELTDHLKDYPTVAVNLODEKCKALMSFLAQWITOL 87
 Db 1 tgdcsfthpsissdfavkirelsdyllqdyptvasnlgdeecgylwrlvlaqrmerl 60
 QY 88 KTVAGSKMOTLEDVNTTEHFVTSCTFOPLPCLRFVQTNISHLKDYCTOLALKPCIG 147
 Db 61 ktvagskmqglilervntelhfvtceafqppscrlfvtgnlsrllgseteqvalxpwlt 120
 QY 148 KACQNSRCLEVOCCPDSTLLPRSPALTELTPEPRRQQLLLDLPLTVLAA 207
 Db 121 r--qnfsrclelqcpdsstlppwsprrpleatlapqp--lllllllpvgllllaaa 176
 QY 208 WGLRMQRRARR---GELHPGVPLP 228
 Db 177 wclhwqtrrrtrprgegyppvp 201

RESULT 24

AAV69725 standard; Protein: 209 AA.

AC AAV69725;
 XX 05-JUL-2000 (first entry)
 DE Human flt-3 mutain W118R.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutain.

OS Homo sapiens.
 OS Synthetic.

PN WO200001823-A2.

PD 13-JAN-2000.
 XX 25-JUN-1999, 99WO-US14296.
 XX 02-JUL-1998, 98US-0109100.

PA (IMNV) IMMUNEX CORP.

XX Gradis TJ, McGrew JT;
 PI WPI; 2000-182115/16.
 XX

PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PR immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122 -
 PS Claim 4: Page 86-87; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibit increased or decreased biological activity relative to
 CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the W118R mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.

SQ Sequence 209 AA;

Query Match 56.0%; Score 685; DB 21; Length 209;
 Best Local Similarity 69.8%; Pred. No. 6.7e-61;
 Matches 143; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

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 QY 148 KACQNSRCLEVOCCPDSTLLPRSPALTELTPEPRRQQLLLDLPLTVLAA 207
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 QY 208 WGLRMQRRARR---GELHPGVPLP 228
 Db 177 wclhwqtrrrtrprgegyppvp 201

RESULT 25

AAV69726 standard; Protein: 209 AA.

AC AAV69726;

XX 05-JUL-2000 (first entry)

DE Human flt-3 mutain Q122R.

XX Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutain.

OS Homo sapiens.
 OS Synthetic.

PN WO200001823-A2.

PD 13-JAN-2000.

XX

Sequence 209 AA;

Matches 14

Db 177 wclhwgrtrrtpgqvpvpsp 201

Job time: 293 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 6, 2002, 09:44:48 ; Search time 201.6 Seconds

(without alignments)
403.311 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223

Sequence: 1 MYTLAPAWSPNSLLILLILL.....WQARRRGELHPCVLPSPHP 231

Scoring table:

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Gapop 10.0 , Capext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	231	1	PCT-US98-12085-2
2	1223	100.0	231	4	US-08-068-394-2
3	1223	100.0	231	5	US-08-106-463-2
4	1223	100.0	231	5	US-08-111-758-2
5	1223	100.0	231	5	US-08-162-407-2
6	1223	100.0	231	8	US-08-444-625-2
7	1223	100.0	231	8	US-08-444-626-2

8	1223	100.0	231	8	US-08-444-632-2	Sequence 2, Appl1
9	1223	100.0	231	10	US-08-669-697-2	Sequence 2, Appl1
10	1223	100.0	231	12	US-08-877-421-2	Sequence 2, Appl1
11	1223	100.0	231	18	US-09-448-378-2	Sequence 2, Appl1
12	1223	100.0	231	18	US-09-629-430B-8	Sequence 8, Appl1
13	1223	100.0	231	20	US-09-629-430B-8	Sequence 2, Appl1
14	1223	100.0	231	23	US-09-629-430B-8	Sequence 2, Appl1
15	1223	100.0	231	24	US-10-095-449-2	Sequence 2, Appl1
16	1212.5	99.1	232	5	US-08-155-111-38	Sequence 38, Appl1
17	1212.5	99.1	232	5	US-08-162-413-38	Sequence 38, Appl1
18	1212.5	99.1	232	6	US-08-261-513-38	Sequence 38, Appl1
19	1212.5	99.1	232	8	US-08-472-168-38	Sequence 38, Appl1
20	1212.5	99.1	232	8	US-08-484-882-38	Sequence 38, Appl1
21	1208.5	98.8	232	8	US-08-486-661-38	Sequence 38, Appl1
22	1006	82.3	286	19	US-09-629-430B-13	Sequence 13, Appl1
23	1006	82.3	287	19	US-09-501-097-25	Sequence 25, Appl1
24	1004	82.1	189	20	US-09-501-097A-25	Sequence 25, Appl1
25	879	71.9	172	20	US-09-629-430B-9	Sequence 9, Appl1
26	879	71.9	220	20	US-09-629-430B-17	Sequence 17, Appl1
27	879	71.9	220	20	US-09-629-430B-11	Sequence 11, Appl1
28	774	63.3	294	17	US-09-322-409-7	Sequence 15, Appl1
29	774	63.3	294	18	US-09-451-527-7	Sequence 7, Appl1
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34	772.5	63.2	235	8	US-08-484-882-34	Sequence 34, Appl1
35	772.5	63.2	235	8	US-08-486-661-34	Sequence 34, Appl1
36	772.5	63.2	235	20	US-09-629-430B-23	Sequence 23, Appl1
37	768.5	62.8	235	1	PCT-US98-12085-4	Sequence 4, Appl1
38	768.5	62.8	235	5	US-08-106-463-6	Sequence 6, Appl1
39	768.5	62.8	235	5	US-08-111-758-6	Sequence 6, Appl1
40	768.5	62.8	235	5	US-08-162-407-6	Sequence 6, Appl1
41	768.5	62.8	235	8	US-08-444-625-6	Sequence 6, Appl1
42	768.5	62.8	235	8	US-08-444-626-6	Sequence 6, Appl1
43	768.5	62.8	235	8	US-08-444-632-6	Sequence 6, Appl1
44	768.5	62.8	235	10	US-08-669-692-6	Sequence 6, Appl1
45	768.5	62.8	235	12	US-08-877-421-4	Sequence 4, Appl1
46	768.5	62.8	235	18	US-09-448-378-1	Sequence 1, Appl1
47	768.5	62.8	235	20	US-09-629-430B-19	Sequence 19, Appl1
48	768.5	62.8	235	22	US-09-891-498-1	Sequence 1, Appl1
49	768.5	62.8	235	23	US-09-904-536-1	Sequence 1, Appl1
50	768.5	62.8	235	23	US-09-983-806-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
Sequence 2, Application PC/TUS9812085
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune To
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, Version 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12085
FILING DATE: 12-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

```

1      REGISTRATION NUMBER: 32,655
2      REFERENCE/DOCKET NUMBER: 2855-WO
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: (206) 587-0430
5      TELEFAX: (206) 233-0644
6      TELEEX: 756822
7      INFORMATION FOR SEQ ID NO: 2:
8      SEQUENCE CHARACTERISTICS:
9      LENGTH: 231 amino acids
10     TYPE: amino acid
11     TOPOLOGY: linear
12     MOLECULE TYPE: protein
13     CDT-US98-12085-2

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Query Match	100.0%;	Score 1223;	DB 1;	Length 231;
Best Local Similarity	100.0%;	Pred. No. 2.7e-110;		
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61 VAVNLQDEHKALMSLFLAORWIEQLKVAGSKMÖTLEDVNTIEIHFVMSCTFQPLPEC 120

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Db 121 LRFVQTNISHLKDCTQLLALPKPCIGKACQNFSRCLEAVQCQPDSSLLPPRSPIALAEAT 180U
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QY 181 ELPEPRRQLLLLLLPLTVLLAAAWGIRWQRARRRGELHPGVLPSPH 231
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Db 181 ELPEPRRQLLLLLLPLTVLLAAAWGIRWQRARRRGELHPGVLPSPH 231

RESULT 2
ITS-08-068-394-2

; Sequence 2, Application 05/08068394
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 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Lyman, Stewart D.
 ;
 ; ADDRESSEE: Beckmann M Patricia

```

; ; TITLE OF INVENTION: Ligands for It3/Itk-2 Receptors
; ; NUMBER OF SEQUENCES: 4
; ; CORRESPONDENCE ADDRESS:
; ; Inventor: Shabaz I. Vojtech, Immunex Corporation

```

```
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: Washington
;
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;
;      ZIP:  98101
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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FILING DATE: 19930524
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:

NAME: Malasaa, Stephen D.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813
TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 387-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO. 2:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: 1 trans

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MOLECULE TYPE: protein
US-08-068-394-2

Query Match	100.0%;	Score 1223;	DB 4;	Length 231;
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DB 1 MTVALPAMSPNSSLLLLLLLSPCLRG⁹PD¹CY⁹SH⁹SP¹SS⁹NF⁹KY⁹KF⁹REL⁹TD¹HL⁹KD⁹PV⁹T 60

[illegible]

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 181 ELPEPPROLILLPLTLVLLAAWGLRWQARRRRGGELHPGPLSPH 231

RESULT 3

Sequence 2, Application US/08106463
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.

```

;
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
;
; NUMBER OF SEQUENCES: 6
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; CORRESPONDENCE ADDRESS:
;

```

STREET: 51 University Street
CITY: Seattle
STATE: Washington

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/ COMM: 00
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/06/100/*
FILING DATE: 19930812
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-7

TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR STD. TD. NO. 3:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
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MOLECULE TYPE: protein
US-08-106-463-2

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; Sequence 2, Application US/08111758
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
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; APPLICATION NUMBER: US/08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-111-758-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
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DB 121 LRFVQTNISHLLKDKCTQTLALKPCIGKACONFSRCLEVOQOPDSSSTLLPPRSPALEAT 180

QY 121 LRFVQTNISHLLKDKCTQTLALKPCIGKACONFSRCLEVOQOPDSSSTLLPPRSPALEAT 180
DB 121 LRFVQTNISHLLKDKCTQTLALKPCIGKACONFSRCLEVOQOPDSSSTLLPPRSPALEAT 180
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DB 181 ELPEPRRQLLLLLLLLPLTLVLAANGLRMQRARRRGELHPGVPLPSHP 231

RESULT 5
US-08-162-407-2
; Sequence 2, Application US/08162407
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-162-407-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MYVLAPAWSPNSLLLLLLLSPCLRGTPDCYFSHSPISNFKVFRRLTDHLKDYPT 60
QY 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
DB 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTQPLPEC 120
QY 121 LRFVQTNISHLLKDKCTQTLALKPCIGKACONFSRCLEVOQOPDSSSTLLPPRSPALEAT 180
DB 121 LRFVQTNISHLLKDKCTQTLALKPCIGKACONFSRCLEVOQOPDSSSTLLPPRSPALEAT 180

Db 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQDPDSSTLLPPRSPITALEAT 180
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RESULT 6

US-08-444-625-2
; Sequence 2, Application US/08444625
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,625
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-625-2

Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAAPAMSNSSLLILLSPCLRGTPDCYFSHSPISNFKYKRELTDLHLKDYPT 60
Db 1 MTVLAAPAMSNSSLLILLSPCLRGTPDCYFSHSPISNFKYKRELTDLHLKDYPT 60
QY 61 VAVNLOERCKALMSLFLAQRWIEQLTVAGSKMOTLLEDVNTTEIHFTVTSCTFOPLPEC 120
Db 61 VAVNLOERCKALMSLFLAQRWIEQLTVAGSKMOTLLEDVNTTEIHFTVTSCTFOPLPEC 120

QY 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQDPDSSTLLPPRSPITALEAT 180
Db 121 LRFVQTNISHLKDTCTQLLAKPCIGKACQNFSCLEVCQDPDSSTLLPPRSPITALEAT 180
QY 181 ELPEPRQQLLLLLLLPLTLVLLAAAGLIRWQARRRGELHPGVLPDSHP 231
Db 181 ELPEPRQQLLLLLLLPLTLVLLAAAGLIRWQARRRGELHPGVLPDSHP 231

RESULT 7

US-08-444-626-2
; Sequence 2, Application US/08444626
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-626-2

Query Match 100.0%; Score 1223; DB 8; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAAPAMSNSSLLILLSPCLRGTPDCYFSHSPISNFKYKRELTDLHLKDYPT 60
Db 1 MTVLAAPAMSNSSLLILLSPCLRGTPDCYFSHSPISNFKYKRELTDLHLKDYPT 60
QY 61 VAVNLOERCKALMSLFLAQRWIEQLTVAGSKMOTLLEDVNTTEIHFTVTSCTFOPLPEC 120
Db 61 VAVNLOERCKALMSLFLAQRWIEQLTVAGSKMOTLLEDVNTTEIHFTVTSCTFOPLPEC 120

Db 61 VAVNLDEKCKALMSLFLAQRIEOLKTVAGSKMOTLLEVDNTEIHVYTSCTFOPLPEC 120
QY 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPRSPRIAEAT 180
Db 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPRSPRIAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLLAAWGLRWQARRRGELHPGVLPSPHP 231
Db 181 ELPEPRRQLLLLLLPLTLVLLAAWGLRWQARRRGELHPGVLPSPHP 231

RESULT 8
US-08-444-632-2
; Sequence 2, Application US/08444632

; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,632
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-444-632-2

Query Match 100.0%; Score 1223; DB 8; Length 231;

Best Local Similarity 100.0%; Pred. No. 2,7e-110; Mismatches 0; Gaps 0;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVIAPAWSPNSLSILLILLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPTV 60
Db 1 MTVIAPAWSPNSLSILLILLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPTV 60

QY 61 VAVNLDEKCKALMSLFLAQRIEOLKTVAGSKMOTLLEVDNTEIHVYTSCTFOPLPEC 120
Db 61 VAVNLDEKCKALMSLFLAQRIEOLKTVAGSKMOTLLEVDNTEIHVYTSCTFOPLPEC 120
QY 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPRSPRIAEAT 180
Db 121 LRFVQINISHLKDTCTQLALPCIGKACONFSRCLEVOQCPDSSSTLLPRSPRIAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLLAAWGLRWQARRRGELHPGVLPSPHP 231
Db 181 ELPEPRRQLLLLLLPLTLVLLAAWGLRWQARRRGELHPGVLPSPHP 231

RESULT 9
US-08-669-692-2
; Sequence 2, Application US/08669692

; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,692
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-669-692-2

Query Match 100.0%; Score 1223; DB 10; Length 231;

Best Local Similarity 100.0%; Pred. No. 2,7e-110; Mismatches 0; Indels 0; Gaps 0;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVIAPAWSPNSLSILLILLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPTV 60
Db 1 MTVIAPAWSPNSLSILLILLSPCLRGTPDCYFSHSPISSNFKVFRRLTDHLKDYPTV 60

OY 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTTEIHFVTSCTFOPLPEC 120
DB 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTTEIHFVTSCTFOPLPEC 120
OY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
OY 181 ELPEPRRQOLLILLILLPLTLVLAAAGLWMORARRRGGELHGVPLPSHP 231
DB 181 ELPEPRRQOLLILLILLPLTLVLAAAGLWMORARRRGGELHGVPLPSHP 231

RESULT 10
US-08-877-421-2
; Sequence 2, Application US/08877421
; GENERAL INFORMATION:
; APPLICANT: Viney, Joanne L.
; APPLICANT: Mowatt, Allan MCI.
; APPLICANT: Abbott, Nicholas
; TITLE OF INVENTION: A Method of Enhancing Antigen-Specific Peripheral Immune Tol
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Macintosh 7.6
; SOFTWARE: Microsoft Word, Version #6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,421
; FILING DATE: 17-JUN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-877-421-2

Query Match 100.0%; Score 1223; DB 12; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 ELPEPRRQOLLILLILLPLTLVLAAAGLWMORARRRGGELHGVPLPSHP 231
RESULT 11
US-09-448-378-2
; Sequence 2, Application US/09448378
; GENERAL INFORMATION:
; APPLICANT: Basel, Kenneth
; TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
; FILE REFERENCE: 2836-D
; CURRENT APPLICATION NUMBER: US/09/448,378
; CURRENT FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-448-378-2

Query Match 100.0%; Score 1223; DB 18; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVLAPAMSPNSLSLLILLISPLCLGTPDCYFSHPISNFKVKFRELTDLHKDYPVT 60
DB 1 MTVLAPAMSPNSLSLLILLISPLCLGTPDCYFSHPISNFKVKFRELTDLHKDYPVT 60
OY 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTTEIHFVTSCTFOPLPEC 120
DB 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTTEIHFVTSCTFOPLPEC 120
OY 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
DB 121 LRFVQTNISHLKDTCTQTLALKPCIGKACONFSRCLEVOCCOPDSSSTLLPPRSPALAEAT 180
OY 181 ELPEPRRQOLLILLILLPLTLVLAAAGLWMORARRRGGELHGVPLPSHP 231
DB 181 ELPEPRRQOLLILLILLPLTLVLAAAGLWMORARRRGGELHGVPLPSHP 231

RESULT 12
US-09-629-430B-8
; Sequence 8, Application US/09629430B
; GENERAL INFORMATION:
; APPLICANT: Hermanson, Gary George
; TITLE OF INVENTION: F1T-3-ligand-Encoding Polynucleotide as a
; TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer
; FILE REFERENCE: 1530.0130001
; CURRENT APPLICATION NUMBER: US/09/629,430B
; CURRENT FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/146,170
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 8
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-629-430B-8

Query Match 100.0%; Score 1223; DB 20; Length 231;
Best Local Similarity 100.0%; Pred. No. 2.7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTVLAPAMSPNSLSLLILLISPLCLGTPDCYFSHPISNFKVKFRELTDLHKDYPVT 60
DB 1 MTVLAPAMSPNSLSLLILLISPLCLGTPDCYFSHPISNFKVKFRELTDLHKDYPVT 60
OY 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTTEIHFVTSCTFOPLPEC 120
DB 61 VAVNLODEKCKALMSLFLAQRWIEOLKTVAGSKMOTLLEDVNTTEIHFVTSCTFOPLPEC 120

Db 61 VAVNIDDEKHCALMSLFLAQRIEOLKTVASGMOTLLEEDVNTIHFVTSCTROPLEPC 120
QY 121 LRFVQTNISHLKDCITQTLALPCIGACQNFSCLEVOQCPDPSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDCITQTLALPCIGACQNFSCLEVOQCPDPSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLPLTVLVAAMGLRQORARRRGEHLHPGVPLPSHP 231
Db 181 ELPEPRRQLLLLLLPLTVLVAAMGLRQORARRRGEHLHPGVPLPSHP 231

RESULT 13

US-09-983-806-2
; Sequence 2, Application US/09983806
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/983,806
; FILING DATE: 25-Oct-2001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,626
; FILING DATE: 19-MAY-1995
; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-983-806-2

Query Match 100.0%; Score 1223; DB 23; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVYKFRRLDHLKDYPT 60
Db 1 MTVLAPAWSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVYKFRRLDHLKDYPT 60

QY 61 VAVNIDDEKHCALMSLFLAQRIEOLKTVASGMOTLLEEDVNTIHFVTSCTROPLEPC 120
Db 61 VAVNIDDEKHCALMSLFLAQRIEOLKTVASGMOTLLEEDVNTIHFVTSCTROPLEPC 120
QY 121 LRFVQTNISHLKDCITQTLALPCIGACQNFSCLEVOQCPDPSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLKDCITQTLALPCIGACQNFSCLEVOQCPDPSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQLLLLLLPLTVLVAAMGLRQORARRRGEHLHPGVPLPSHP 231
Db 181 ELPEPRRQLLLLLLPLTVLVAAMGLRQORARRRGEHLHPGVPLPSHP 231

RESULT 14

US-10-095-449-2
; Sequence 2, Application US/10095449
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/095,449
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/669,692
; FILING DATE: 24-JUN-1996
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-095-449-2

Query Match 100.0%; Score 1223; DB 24; Length 231;
Best Local Similarity 100.0%; Pred. No. 2,7e-110;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAWSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVYKFRRLDHLKDYPT 60
Db 1 MTVLAPAWSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVYKFRRLDHLKDYPT 60

Db 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTILEVDNTEIHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLLKDTCTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLLKDTCTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRPRO-LILLILLPLTLVLLAAAGLRWQARRRGELHPVPLPSHP 231
Db 181 ELPEPRPRO-LILLILLPLTLVLLAAAGLRWQARRRGELHPVPLPSHP 232

RESULT 17
US-08-261-553-38

/ Sequence 38, Application US/08261553
/ GENERAL INFORMATION:
/ APPLICANT: Hannum, Charles H.
/ APPLICANT: Culpepper, Janice A.
/ APPLICANT: Lee, Frank D.
/ APPLICANT: Birdaun, Daniel
/ TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: DNAX Research Institute
/ STREET: 901 California Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/261,553
/ FILING DATE: 17-JUN-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/162,413
/ FILING DATE: 03-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/155,111
/ FILING DATE: 19-NOV-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/112,391
/ FILING DATE: 24-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/106,340
/ FILING DATE: 13-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/089,263
/ FILING DATE: 07-JUL-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/065,231
/ FILING DATE: 19-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ching, Edwin P.
/ REGISTRATION NUMBER: 34,090
/ REFERENCE/DOCKET NUMBER: DX0350K7
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-852-9196
/ TELEFAX: 415-496-1200
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 232 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-261-553-38

Query Match

99.1%; Score 1212.5; DB 6; Length 232;

Best Local Similarity 99.6%; Pred. No. 2.8e-109;
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MIVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKYKFEILDHLKDPYV 60
Db 1 MIVLAPAMSPNSLLILLLLSPCLRGTPDCYFSHSPISSNFKYKFEILDHLKDPYV 60
QY 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTILEVDNTEIHFVTSCTFQPLPEC 120
Db 61 VAVNIODEKHCKALMSLFLAQRWIEQLKTVAGSKMOTILEVDNTEIHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLLKDTCTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
Db 121 LRFVQTNISHLLKDTCTQLALKPCIGKACQNFSCRLEVOQCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRPRO-LILLILLPLTLVLLAAAGLRWQARRRGELHPVPLPSHP 231
Db 181 ELPEPRPRO-LILLILLPLTLVLLAAAGLRWQARRRGELHPVPLPSHP 232

RESULT 18
US-08-472-168-38

/ Sequence 38, Application US/08472168
/ GENERAL INFORMATION:
/ APPLICANT: Hannum, Charles H.
/ APPLICANT: Culpepper, Janice A.
/ APPLICANT: Lee, Frank D.
/ APPLICANT: Birdaun, Daniel
/ TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
/ NUMBER OF SEQUENCES: 42
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: DNAX Research Institute
/ STREET: 901 California Avenue
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304-1104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/472,168
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/261,553
/ FILING DATE: 17-JUN-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/162,413
/ FILING DATE: 03-DEC-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/155,111
/ FILING DATE: 19-NOV-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/112,391
/ FILING DATE: 24-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/106,340
/ FILING DATE: 13-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/089,263
/ FILING DATE: 07-JUL-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/065,231
/ FILING DATE: 19-MAY-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ching, Edwin P.
/ REGISTRATION NUMBER: 34,090
/ REFERENCE/DOCKET NUMBER: DX0350K7
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-852-9196

TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-168-38

Query Match 99.1%; Score 1212.5; DB 8; Length 232;
Best Local Similarity 99.6%; Pred. No. 2.8e-109;
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDHLKDYPT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEQLKTAVGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
DB 61 VAVNLQDEKHKALMSFLAQRWIEQLKTAVGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRPRO-LLILLPLTLVLLAAMGLRMQARRRGELHGVPLPSHP 231
DB 181 ELPEPRPRO-LLILLPLTLVLLAAMGLRMQARRRGELHGVPLPSHP 232

RESULT 19
US-08-484-882-38
Sequence 38, Application US/08484882

GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
APPLICANT: Birnbaum, Daniel
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
NUMBER OF SEQUENCES: 42
TITLE OF INVENTION: AGONISTS; ANTAGONISTS
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,553
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0350K7GD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-882-38

Query Match 99.1%; Score 1212.5; DB 8; Length 232;
Best Local Similarity 99.6%; Pred. No. 2.8e-109;
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSSHSPISSENFVKYKRELTDHLKDYPT 60
QY 61 VAVNLQDEKHKALMSFLAQRWIEQLKTAVGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
DB 61 VAVNLQDEKHKALMSFLAQRWIEQLKTAVGSKMOTLLEDVNTETHEFTVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACQNFSCLEVOCCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRPRO-LLILLPLTLVLLAAMGLRMQARRRGELHGVPLPSHP 231
DB 181 ELPEPRPRO-LLILLPLTLVLLAAMGLRMQARRRGELHGVPLPSHP 232

RESULT 20
US-08-486-661-38

Sequence 38, Application US/08486661
GENERAL INFORMATION:
APPLICANT: Hannum, Charles H.
APPLICANT: Culpepper, Janice A.
APPLICANT: Lee, Frank D.
APPLICANT: Birnbaum, Daniel
TITLE OF INVENTION: PURIFIED MAMMALIAN FLT3 LIGANDS;
NUMBER OF SEQUENCES: 42
TITLE OF INVENTION: AGONISTS; ANTAGONISTS
CORRESPONDENCE ADDRESS:
ADDRESS: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,661
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0350K7GC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: 1linear
MOLECULE TYPE: protein
US-08-486-661-38

Query Match 99.1%; Score 1212.5; DB 8; Length 232;
Best Local Similarity 99.6%; Pred. No. 2.8e-109;
Matches 231; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120
QY 121 LRFVQNTISHLKDTCTQLALPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQNTISHLKDTCTQLALPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQQLTLTLPLTVLLAAAGLWQARRRGELHPVPLPSHP 231
DB 181 ELPEPRRQQLTLTLPLTVLLAAAGLWQARRRGELHPVPLPSHP 232

RESULT 21
US-09-629-430B-13
Sequence 13, Application US/09629430B
GENERAL INFORMATION:
APPLICANT: Hermanson, Gary George
TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as a
TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer
FILE REFERENCE: 1530.0130001
CURRENT APPLICATION NUMBER: US/09/629,430B
CURRENT FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/146,170
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 232
TYPE: PRT
ORGANISM: Mus musculus
US-09-629-430B-13

Query Match 98.8%; Score 1208.5; DB 20; Length 232;
Best Local Similarity 99.1%; Pred. No. 7e-109;
Matches 230; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120
QY 121 LRFVQNTISHLKDTCTQLALPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQNTISHLKDTCTQLALPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQQLTLTLPLTVLLAAAGLWQARRRGELHPVPLPSHP 231
DB 181 ELPEPRRQQLTLTLPLTVLLAAAGLWQARRRGELHPVPLPSHP 231

DB 181 ELPEPRRQQLTLTLPLTVLLAAAGLWQARRRGELHPVPLPSHP 232

RESULT 22
US-09-501-097-25
Sequence 25, Application US/09501097
GENERAL INFORMATION:
APPLICANT: Tzyy-Chou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 02240-169349
CURRENT APPLICATION NUMBER: US/09/501,097
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 286
TYPE: PRT
ORGANISM: Human papillomavirus/Mouse
US-09-501-097-25

Query Match 82.3%; Score 1006; DB 19; Length 286;
Best Local Similarity 99.5%; Pred. No. 4.9e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120
QY 121 LRFVQNTISHLKDTCTQLALPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
DB 121 LRFVQNTISHLKDTCTQLALPCIGKACQNFSCLEVOCPDSSSTLLPPRSPIALEAT 180
QY 181 ELPEPRRQQL 190
DB 181 ELPEPRRQQL 190

RESULT 23
US-09-501-097A-25
Sequence 25, Application US/09501097A
GENERAL INFORMATION:
APPLICANT: Tzyy-Chou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 287
TYPE: PRT
ORGANISM: Human papillomavirus/Mouse
US-09-501-097A-25

Query Match 82.3%; Score 1006; DB 19; Length 287;
Best Local Similarity 99.5%; Pred. No. 4.9e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
DB 1 MTVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNKVKFRELTDHLKDYPT 60
QY 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120
DB 61 VAVNLDEKHCALMSLFLAQRWIEQLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLEC 120

Tue Aug 6 09:34:38 2002

us-09-448-378-2.rapm

Page 13

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:41:14 ; Search time 38.79 Seconds
(without alignments)
899.284 Million cell updates/sec

Title: US-09-448-378-2
Perfect score: 1223
Sequence: 1 MVLAPAMSPNSLLILL.....WQARRRGELHPGVLPSPH 231

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 463719 seqs, 15109603 residues

Total number of hits satisfying chosen parameters: 463719

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/pdata/1/paa/US06_NEM_COMB.pep:*
3: /cgn2_6/pdata/1/paa/US07_NEM_COMB.pep:*
4: /cgn2_6/pdata/1/paa/US08_NEM_COMB.pep:*
5: /cgn2_6/pdata/1/paa/US09_NEM_COMB.pep:*
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7: /cgn2_6/pdata/1/paa/US60_NEM_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1223	100.0	231	7 US-60-368-263-2	Sequence 2, Appl 1
2	768.5	62.8	235	1 PCT-US02-20172-4	Sequence 4, Appl 1
3	768.5	62.8	235	7 US-60-368-263-1	Sequence 1, Appl 1
4	763.5	62.4	235	1 PCT-US02-20172-5	Sequence 5, Appl 1
5	568	46.4	156	6 US-10-053-355A-1	Sequence 1, Appl 1
6	565.5	46.2	189	1 PCT-US02-20172-2	Sequence 2, Appl 1
7	89.5	7.3	941	7 US-60-389-987-2466	Sequence 2466, Ap
8	88	7.2	1928	1 PCT-US02-18507-30	Sequence 30, Appl
9	88	7.2	1966	1 PCT-US02-18507-6	Sequence 2, Appl 1
10	88	7.2	1966	1 PCT-US02-18507-2	Sequence 6, Appl 1
11	88	7.2	1966	1 PCT-US02-18507-8	Sequence 8, Appl 1
12	88	7.2	1966	1 PCT-US02-18507-10	Sequence 10, Appl
13	88	7.2	1966	1 PCT-US02-18507-12	Sequence 12, Appl
14	88	7.2	1966	1 PCT-US02-18507-14	Sequence 14, Appl
15	88	7.2	1966	1 PCT-US02-18507-16	Sequence 16, Appl
16	88	7.2	1966	1 PCT-US02-18507-18	Sequence 18, Appl
17	88	7.2	1966	1 PCT-US02-18507-20	Sequence 20, Appl
18	88	7.2	1966	1 PCT-US02-18507-22	Sequence 22, Appl
19	88	7.2	1966	1 PCT-US02-18507-24	Sequence 24, Appl
20	88	7.2	1966	1 PCT-US02-18507-26	Sequence 26, Appl
21	88	7.2	1966	1 PCT-US02-18507-28	Sequence 28, Appl
22	84.5	6.9	1205	1 PCT-US02-18211-1	Sequence 1, Appl 1
23	84.5	6.9	1205	1 PCT-US02-18221-1	Sequence 1, Appl 1
24	84.5	6.9	1205	1 PCT-US02-18221-1	Sequence 1, Appl 1
25	83.5	6.8	425	6 US-10-164-890-1	Sequence 35, Appl
26	82.5	6.7	1266	5 US-09-011-307-12	Sequence 12, Appl

27	81.5	6.7	659	5 US-09-629-469A-14346	Sequence 14346, A
28	81.5	6.7	1148	7 US-60-389-987-1068	Sequence 1068, Ap
29	81	6.6	1965	1 PCT-US02-18507-4	Sequence 4, Appl 1
30	81	6.6	4131	7 US-60-360-039-5136	Sequence 5136, Ap
31	80	6.5	245	5 US-09-629-469A-18532	Sequence 18532, A
32	80	6.5	811	5 US-09-991-150-57	Sequence 57, Appl
33	80	6.5	811	5 US-09-950-041-39	Sequence 39, Appl
34	80	6.5	811	5 US-10-121-062-414	Sequence 414, App
35	80	6.5	811	6 US-10-095-627-13	Sequence 13, Appl
36	80	6.5	811	6 US-10-173-699-414	Sequence 414, App
37	80	6.5	811	6 US-10-173-699-414	Sequence 414, App
38	80	6.5	811	6 US-10-173-691-414	Sequence 414, App
39	80	6.5	811	6 US-10-173-692-414	Sequence 414, App
40	80	6.5	811	6 US-10-173-692-414	Sequence 414, App
41	80	6.5	811	6 US-10-173-697-414	Sequence 414, App
42	80	6.5	811	6 US-10-173-698-414	Sequence 414, App
43	80	6.5	811	6 US-10-173-699-414	Sequence 414, App
44	80	6.5	811	6 US-10-173-701-414	Sequence 414, App
45	80	6.5	811	6 US-10-173-704-414	Sequence 414, App
46	80	6.5	811	6 US-10-173-708-414	Sequence 414, App
47	80	6.5	811	6 US-10-174-571-414	Sequence 414, App
48	80	6.5	811	6 US-10-174-574-414	Sequence 414, App
49	80	6.5	811	6 US-10-174-583-414	Sequence 414, App
50	80	6.5	811	6 US-10-173-694-414	Sequence 414, App

ALIGNMENTS

RESULT 1
US-60-368-263-2
; Sequence 2, Application US/60368263
; GENERAL INFORMATION:
; APPLICANT: McKenna, Hilary J.
; APPLICANT: Liebowitz, David N.
; APPLICANT: Maliszewski, Charles R.
; TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
; FILE REFERENCE: 3399
; CURRENT APPLICATION NUMBER: US/60/368, 263
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Mus sp
US-60-368-263-2

Query Match 100.0%; Score 1223; DB 7; Length 231;
Best local Similarity 100.0%; Pred. No. 2e-105;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVLAPAMSPNSLLILLSPCLRGTPDCYFSSPISSNFKYKFRRLDHLKDYPT 60
|||||
Db 1 MVLAPAMSPNSLLILLSPCLRGTPDCYFSHSPISSNFKYKFRRLDHLKDYPT 60
QY 61 VAVNLDKHCALMSFLAORNIOLKTVAISKQOTLLEVNTEIHVTSCTFOPPEC 120
|||||
Db 61 VAVNLDKHCALMSFLAORNIOLKTVAISKQOTLLEVNTEIHVTSCTFOPPEC 120
QY 121 LRFVQNIHLKDKTQTLALPCIGRAQCNFSCLVEQCPDPSSTLLPRSPALEAT 180
|||||
Db 121 LRFVQNIHLKDKTQTLALPCIGRAQCNFSCLVEQCPDPSSTLLPRSPALEAT 180
QY 181 ELPEPRROLILLTLPTLVILAAAGIMQARRRGELHPGVLPSPH 231
|||||
Db 181 ELPEPRROLILLTLPTLVILAAAGIMQARRRGELHPGVLPSPH 231
RESULT 2
PCT-US02-20172-4
; Sequence 4, Application PC/TUS0220172

```

: GENERAL INFORMATION:
: APPLICANT: GONG, Fangcheng et al.
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL001244
: CURRENT APPLICATION NUMBER: PCT/US02/20172
: CURRENT FILING DATE: 2002-06-25
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Human
PCT-US02-20172-4
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Query Match          62.8%; Score 768.5; DB 1; Length 235;
Best Local Similarity 70.3%; Pred. No. 2.5e-63;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
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QY 1 MTVALPAMSPNSLLLLLSPLCRGTPDCYFSPHSPISSNFKVRFRETDHLKDYPT 60
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 MTVALPAMSP--TYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDVLLQDYPVT 59
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QY 61 VAVNLQDEKCKALMSLFLAORWTEOLKTVAAGSKMOTLLEDVNTETLHFVTSCTFQPLPEC 120
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Db 60 VASNLQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGLERVTETLHFVTKCAFQPPSC 119
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QY 121 LRFVQTNISHLKDTCTQTLALPKPCIGKACONFSRCLEVOCCPDSSTLLPPRSPIALEAT 180
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 120 LRFVQTNISRLQETSQTLVALKFWITR--QNFSCRLELCQCPDSSTLPPRPSPIALEAT 177
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 181 ELPRPRROLLLLPLTVLLAAWGLRMQRRAR---GELHPGVPLP 228
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 178 APTAPQPP--LLLLLPVGLLLAAWGLHMQRTRRRPRPEQVPVPSP 227
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```

```

RESULT 3
US-60-368-263-1
: Sequence 1, Application US/60368263
: GENERAL INFORMATION:
: APPLICANT: McKenna, Hilary J.
: APPLICANT: Liebowitz, David N.
: APPLICANT: Maliszewski, Charles R.
: TITLE OF INVENTION: METHODS OF USING FLT-3 LIGAND IN IMMUNIZATION PROTOCOLS
: FILE REFERENCE: 3399
: CURRENT APPLICATION NUMBER: US/60/368,263
: CURRENT FILING DATE: 2002-03-26
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Homo sapiens
US-60-368-263-1
```

```

Query Match          62.8%; Score 768.5; DB 7; Length 235;
Best Local Similarity 70.3%; Pred. No. 2.5e-63;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;
```

```

QY 1 MTVALPAMSPNSLLLLLSPLCRGTPDCYFSPHSPISSNFKVRFRETDHLKDYPT 60
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 MTVALPAMSP--TYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDVLLQDYPVT 59
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 61 VAVNLQDEKCKALMSLFLAORWTEOLKTVAAGSKMOTLLEDVNTETLHFVTSCTFQPLPEC 120
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 60 VASNLQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGLERVTETLHFVTKCAFQPPSC 119
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 121 LRFVQTNISHLKDTCTQTLALPKPCIGKACONFSRCLEVOCCPDSSTLLPPRSPIALEAT 180
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 120 LRFVQTNISRLQETSQTLVALKFWITR--QNFSCRLELCQCPDSSTLPPRPSPIALEAT 177
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
```

```

QY 181 ELPRPRROLLLLPLTVLLAAWGLRMQRRAR---GELHPGVPLP 228
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 178 APTAPQPP--LLLLLPVGLLLAAWGLHMQRTRRRPRPEQVPVPSP 227
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
```

```

RESULT 4
PCT-US02-20172-5
: Sequence 5, Application PC/TUS0220172
: GENERAL INFORMATION:
: APPLICANT: GONG, Fangcheng et al.
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL001244
: CURRENT APPLICATION NUMBER: PCT/US02/20172
: CURRENT FILING DATE: 2002-06-25
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Human
PCT-US02-20172-5
```

```

Query Match          62.4%; Score 763.5; DB 1; Length 235;
Best Local Similarity 69.8%; Pred. No. 7.2e-63;
Matches 162; Conservative 17; Mismatches 44; Indels 9; Gaps 4;
```

```

QY 1 MTVALPAMSPNSLLLLLSPLCRGTPDCYFSPHSPISSNFKVRFRETDHLKDYPT 60
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 1 MTVALPAMSP--TYLLLLLSGLSGTQDCSFQHSPISSDFAVKIRELSDVLLQDYPVT 59
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 61 VAVNLQDEKCKALMSLFLAORWTEOLKTVAAGSKMOTLLEDVNTETLHFVTSCTFQPLPEC 120
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 60 VASNLQDEELCGGLMRVLVAQRMMERLKTVAAGSKMGLERVTETLHFVTKCAFQPPSC 119
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 121 LRFVQTNISHLKDTCTQTLALPKPCIGKACONFSRCLEVOCCPDSSTLLPPRSPIALEAT 180
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 120 LRFVQTNISRLQETSQTLVALKFWITR--QNFSCRLELCQCPDSSTLPPRPSPIALEAT 177
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 181 ELPRPRROLLLLPLTVLLAAWGLRMQRRAR---GELHPGVPLP 228
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 178 APTAPQPP--LLLLLPVGLLLAAWGLHMQRTRRRPRPEQVPVPSP 227
    ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
```

```

RESULT 5
US-10-053-355A-1
: Sequence 1, Application US/10053355A
: GENERAL INFORMATION:
: APPLICANT: Rossi, Alex
: TITLE OF INVENTION: Production of Cultured Human Mast Cells and Basophils for High
: TITLE OF INVENTION: Small Molecule Drug Discovery
: FILE REFERENCE: A-70682/RMS/AMS
: CURRENT APPLICATION NUMBER: US/10/053,355A
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: US 60/316,723
: PRIOR FILING DATE: 2001-08-31
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1
: LENGTH: 156
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-053-355A-1
```

```

Query Match          46.4%; Score 568; DB 6; Length 156;
Best Local Similarity 73.9%; Pred. No. 5.5e-45;
Matches 113; Conservative 12; Mismatches 26; Indels 2; Gaps 1;
```

```

QY 28 TPDCTFSPHSPISSNFKVRFRETDHLKDYPTVAVNLQDEKCKALMSLFLAORWTEOL 87
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-2466

Query Match
Best Local Similarity 7.3%; Score 89.5; DB 7; Length 941;
Matches 24; Conservative 0; Mismatches 16; Indels 9; Gaps 2;

OY 148 KACONFSCLEVOCCOPDSTLLPPRSPALFAT 180
DB 122 R-QNFSRCLELOCOPDSTLLPPRSPALFAT 152
```

```

RESULT 6
PCT-US02-20172-2
; Sequence 2, Application PC/TUS0220172
; GENERAL INFORMATION:
; APPLICANT: GONG, Fangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001244
; CURRENT APPLICATION NUMBER: PCT/US02/20172
; CURRENT FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Human
PCT-US02-20172-2
```

```

Query Match
Best Local Similarity 46.2%; Score 565.5; DB 1; Length 189;
Matches 129; Conservative 12; Mismatches 36; Indels 55; Gaps 4;

OY 1 MTVIAPAMSPSSLLILLISCLRGPDYCFHSPTSSNFKVFRRLTDHLKDYPT 60
DB 1 MTVIAPAMSP-TTYLLILLISLSSGLSTGDCSFQSPSSDPAVKIRLSYLLQDYPVT 59
OY 61 VAVNLODEKCKALMSFLAQRNIEQLKTVAGSKMOTLLEDVNTFHFVTSCTQPLPEC 120
DB 60 VASINLODEELCGGLMRLVLAQRNMRKLTAVAGSKMOTLLEDVNTFHFVTSCTQPLPEC 114
OY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCOPDSTLLPPRSPALFAT 180
DB 115 -----DSTLLPPRSPALFAT 131
OY 181 ELPPRRQQLLLPLTLVLLAANGLRQGRARR-----GELHPCVPLP 228
DB 132 APTAPQPP-TLLTLPLVGLLLAAMCLHMQRTRRTPRPGEQVPPVPS 181
```

```

RESULT 7
US-60-389-987-2466
; Sequence 2466, Application US/60389987
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fany, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660098.465P2
; CURRENT APPLICATION NUMBER: US/60/389,987
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2466
; LENGTH: 941
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-2466
```

```

Query Match
Best Local Similarity 7.3%; Score 89.5; DB 7; Length 941;
Matches 24; Conservative 0; Mismatches 16; Indels 9; Gaps 2;

OY 183 PEPPRQLLLPLTLVLLAANGLRQGRARRGELHPCVPLPSHP 231
DB 15 PPPPPARLLLLPLLLPLIAPGAMG--WANGARR-----PPPS 54
```

```

RESULT 8
PCT-US02-18507-30
; Sequence 30, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004W0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 1928
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-30
```

```

Query Match
Best Local Similarity 7.2%; Score 88; DB 1; Length 1928;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

OY 27 GTPCCYSHSPSSNFKVFRRLTDHLK---DYPTVAVNLODEKCKALM-----STFL 79
DB 139 GVPD-----NLSFYK-----NHIMKRYDRPHKGT-KDENEFKSLMERTSYL 1445
OY 80 AQ-----RW-IEQLKTVAGSKMOT--LLEDVNTFHFVTSCTQPLPEC 121
DB 1446 VQSLPGISRMFEVEKREYVMSPLFNALIVLENNKQQLKTLISQOTROMQINPLTMCL 1505
OY 122 -----RFV 124
DB 1506 NGVIDAANGVSRQCAFVYKTYILSHPEDGKTIARLEMLDQAQTLFGLAVHKEFY 1565
OY 125 QTNISHLKDTCTQLALKPCIGKACONFSRCLEVO-----CQ-----PDS 165
DB 1566 PQDMRPLHKLVDPQFVYMKSSLG--IOEFSACMQASPVHFPNGSPRYCRNSAPASVDPG 1623
OY 166 STLLPPRSPALFA 179
DB 1624 TRVTPRRSPALSYA 1637
```

```

RESULT 9
PCT-US02-18507-2
; Sequence 2, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004W0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
```

```

; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-us02-18507-2

```

```

Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

```

```

OY 27 GTPDCYFSHSPISSNKFKFRELTDHLK---DYPVYAVNLQDEKCKALM-----SLFL 79
Db 1399 GVPD-----NIKSFYKV-----NHMKFRYDRPFHKGTR-DKENEFKSLWERTSYL 1445
OY 80 AQ-----RW--IEQLKTVAGSKMOT---LLEDVNTTEIH-FVYSC-----TFQPLPECL 121
Db 1446 VQSLPGISRWFEVERKEVEMSPLENALIEVLNNQOLKTLISQCCQROMQINPLTMCL 1505
OY 122 -----REV 124
Db 1506 NGVIDAANGVSRQEAFFVEKEYILSHPEDEKIALRLRELMEOAILFGLAVHEKRV 1565
OY 125 QTNISHLKDTCTQLLAKPCIGKACQNFSCRLEVO-----CQ-----PDS 165
Db 1566 PQDMRPLHKKLVDOFVYMKSSIG--IQEFSACMQASPVHPNGSPRYCGRNSAPASVSPDG 1623
OY 166 STILLPRSPALAE 179
Db 1624 TRVIPRSPSLXPA 1637

RESULT 10
PCT-us02-18507-6
; Sequence 6, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Dock 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004W0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-us02-18507-6

```

```

Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

```

```

OY 27 GTPDCYFSHSPISSNKFKFRELTDHLK---DYPVYAVNLQDEKCKALM-----SLFL 79
Db 1399 GVPD-----NIKSFYKV-----NHMKFRYDRPFHKGTR-DKENEFKSLWERTSYL 1445
OY 80 AQ-----RW--IEQLKTVAGSKMOT---LLEDVNTTEIH-FVYSC-----TFQPLPECL 121
Db 1446 VQSLPGISRWFEVERKEVEMSPLENALIEVLNNQOLKTLISQCCQROMQINPLTMCL 1505
OY 122 -----REV 124
Db 1506 NGVIDAANGVSRQEAFFVEKEYILSHPEDEKIALRLRELMEOAILFGLAVHEKRV 1565
OY 125 QTNISHLKDTCTQLLAKPCIGKACQNFSCRLEVO-----CQ-----PDS 165
Db 1566 PQDMRPLHKKLVDOFVYMKSSIG--IQEFSACMQASPVHPNGSPRYCGRNSAPASVSPDG 1623
OY 166 STILLPRSPALAE 179

```

```

Db 1624 TRVIPRSPSLXPA 1637

```

```

RESULT 11
PCT-us02-18507-8
; Sequence 8, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Dock 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004W0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-us02-18507-8

```

```

Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

```

```

OY 27 GTPDCYFSHSPISSNKFKFRELTDHLK---DYPVYAVNLQDEKCKALM-----SLFL 79
Db 1399 GVPD-----NIKSFYKV-----NHMKFRYDRPFHKGTR-DKENEFKSLWERTSYL 1445
OY 80 AQ-----RW--IEQLKTVAGSKMOT---LLEDVNTTEIH-FVYSC-----TFQPLPECL 121
Db 1446 VQSLPGISRWFEVERKEVEMSPLENALIEVLNNQOLKTLISQCCQROMQINPLTMCL 1505
OY 122 -----REV 124
Db 1506 NGVIDAANGVSRQEAFFVEKEYILSHPEDEKIALRLRELMEOAILFGLAVHEKRV 1565
OY 125 QTNISHLKDTCTQLLAKPCIGKACQNFSCRLEVO-----CQ-----PDS 165
Db 1566 PQDMRPLHKKLVDOFVYMKSSIG--IQEFSACMQASPVHPNGSPRYCGRNSAPASVSPDG 1623
OY 166 STILLPRSPALAE 179
Db 1624 TRVIPRSPSLXPA 1637

```

```

RESULT 12
PCT-us02-18507-10
; Sequence 10, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: Dock 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004W0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-us02-18507-10

```

```

Query Match          7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
OY 27 GTPDCYFSHSPISSNKFKFRELTDHLK---DYPVYAVNLQDEKCKALM-----SLFL 79

```

```
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--TEOLKTAVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VOSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISOCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIISHPEDGEKIALRLBELMEQAQILLEGFLAVHEKVF 1565
QY 125 QTNISHLKDTCTQLALPKCIGKACQNFSCLEVO-----CO-----PDS 165
Db 1566 PODMRPLHKRLVQDFVFMKSLG--IQEFSACQASPVHFPNGSPRVCRNSAPASVSPDG 1623
QY 166 STLPPRSPIALRA 179
Db 1624 TRVIPRRSPLSYPA 1637

RESULT 13
PCT-US02-18507-12
; Sequence 12, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-12

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GTPDCYFHSHPISSNFKVFKRELTDHLK---DYPTAVANLQDEKHKALW-----SLFL 79
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--TEOLKTAVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VOSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISOCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIISHPEDGEKIALRLBELMEQAQILLEGFLAVHEKVF 1565
QY 125 QTNISHLKDTCTQLALPKCIGKACQNFSCLEVO-----CO-----PDS 165
Db 1566 PODMRPLHKRLVQDFVFMKSLG--IQEFSACQASPVHFPNGSPRVCRNSAPASVSPDG 1623
QY 166 STLPPRSPIALRA 179
Db 1624 TRVIPRRSPLSYPA 1637

RESULT 14
PCT-US02-18507-14
; Sequence 14, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
```

```
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-14

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GTPDCYFHSHPISSNFKVFKRELTDHLK---DYPTAVANLQDEKHKALW-----SLFL 79
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--TEOLKTAVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VOSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISOCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIISHPEDGEKIALRLBELMEQAQILLEGFLAVHEKVF 1565

RESULT 15
PCT-US02-18507-16
; Sequence 16, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004WO
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/297,382
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-16

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;

QY 27 GTPDCYFHSHPISSNFKVFKRELTDHLK---DYPTAVANLQDEKHKALW-----SLFL 79
Db 1399 GVPD-----NKSFKV-----NHIMKFRYDRPHKGT-KDENEKSLWERTSLYL 1445
QY 80 AQ-----RW--TEOLKTAVAGSKMOT---LLEDVNTTEIH-FVYTSQ-----TFOPLEPCL 121
Db 1446 VOSLPGISRWFEVEKREVEVMSPLENAIEVLNKNQOLKTLISOCOTROMONINPLTWCL 1505
QY 122 -----REV 124
Db 1506 NGVIDAANGVSRYOAEAFVKEYIISHPEDGEKIALRLBELMEQAQILLEGFLAVHEKVF 1565
```



```

;
; Sequence 24, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004M0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-24
```

```

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
```

```

QY 27 GTPDCYSHSPISNFKRELTDHLK---DYPTAVANIODEKHKALM---SLEFL 79
D 1399 GVPD-----NKSFTYV-----NHIMKFRIDRPHKGTK-DKENEEKSLWVERTSLYL 1445
QY 80 AQ-----RW-TEOLKTAVAGSKMOT---LLEDVNTETIH-FVYSC-----TFOPUPECL 121
D 1446 VQSLPGISRWFEVEKREVEVMSPLENAIEVLENNKQOLKTLISQCOTROMONINPLTMCL 1505
QY 122 -----REV 124
D 1506 NGVIDAANGVSRYOEAFFVKEYILSHPEDGEKIARLRLEMLBOAQILLEGGLAVHEKRV 1565
QY 125 QTNISHLKDTCTQLALAPCIGKACQNFSCLEVO-----CQ-----PDS 165
D 1566 PQDMRPLHKLVQDFVWKMSSLG--IQEFSACMQASPVHFPNGSPRYCNSAPASVSPDG 1623
QY 166 STLLPPRSPIALEA 179
D 1624 TRVIPRRSPPLSTPA 1637

RESULT 20
PCT-US02-18507-26
; Sequence 26, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004M0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-26
```

```

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
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```

D 1446 VQSLPGISRWFEVEKREVEVMSPLENAIEVLENNKQOLKTLISQCOTROMONINPLTMCL 1505
QY 122 -----REV 124
D 1506 NGVIDAANGVSRYOEAFFVKEYILSHPEDGEKIARLRLEMLBOAQILLEGGLAVHEKRV 1565
QY 125 QTNISHLKDTCTQLALAPCIGKACQNFSCLEVO-----CQ-----PDS 165
D 1566 PQDMRPLHKLVQDFVWKMSSLG--IQEFSACMQASPVHFPNGSPRYCNSAPASVSPDG 1623
QY 166 STLLPPRSPIALEA 179
D 1624 TRVIPRRSPPLSTPA 1637
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RESULT 21
PCT-US02-18507-28
; Sequence 28, Application PC/TUS0218507
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: DOCK 3 Tumor Suppressor Gene
; FILE REFERENCE: M01053/70004M0
; CURRENT APPLICATION NUMBER: PCT/US02/18507
; CURRENT FILING DATE: 2002-06-10
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1966
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-18507-28

Query Match 7.2%; Score 88; DB 1; Length 1966;
Best Local Similarity 20.1%; Pred. No. 35;
Matches 51; Conservative 29; Mismatches 58; Indels 116; Gaps 14;
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QY 27 GTPDCYSHSPISNFKRELTDHLK---DYPTAVANIODEKHKALM---SLEFL 79
D 1399 GVPD-----NKSFTYV-----NHIMKFRIDRPHKGTK-DKENEEKSLWVERTSLYL 1445
QY 80 AQ-----RW-TEOLKTAVAGSKMOT---LLEDVNTETIH-FVYSC-----TFOPUPECL 121
D 1446 VQSLPGISRWFEVEKREVEVMSPLENAIEVLENNKQOLKTLISQCOTROMONINPLTMCL 1505
QY 122 -----REV 124
D 1506 NGVIDAANGVSRYOEAFFVKEYILSHPEDGEKIARLRLEMLBOAQILLEGGLAVHEKRV 1565
QY 125 QTNISHLKDTCTQLALAPCIGKACQNFSCLEVO-----CQ-----PDS 165
D 1566 PQDMRPLHKLVQDFVWKMSSLG--IQEFSACMQASPVHFPNGSPRYCNSAPASVSPDG 1623
QY 166 STLLPPRSPIALEA 179
D 1624 TRVIPRRSPPLSTPA 1637

RESULT 22
PCT-US02-18211-1
; Sequence 1, Application PC/TUS0218211
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel S.
; APPLICANT: Hirohata, Satoshi
; APPLICANT: Eyre, David
; APPLICANT: Bernades, Russell
; TITLE OF INVENTION: ADAMTS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: 26336-10-1
; CURRENT APPLICATION NUMBER: PCT/US02/18211
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/296,384
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Tue Aug, 6 09:34:39 2002

us-09-448-378-2.rapn

Page 9

Best Local Similarity 19.6%; Pred. No. 14;
Matches 51; Conservative 34; Mismatches 72; Indels 103; Gaps 12;

[illegible]

Search completed: August 6, 2002, 09:41:16
Job time: 227 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 09:39:37 ; Search time 22.73 seconds

(without alignments)
248.232 Million cell updates/sec

Title: US-09-448-378-2

Perfect score: 1223
Sequence: 1 MVLAPAMSPNSLLILL.....MQRARRGELHPGVLPSPHP 231

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
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5: /cgn2_6/prodata/2/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1223	100.0	231	1	US-08-243-545-2
2	1223	100.0	231	2	US-08-993-962-2
3	1223	100.0	231	4	US-09-160-841-2
4	1223	100.0	231	5	PCT-US94-05365-2
5	1220	99.8	231	1	US-08-220-379B-7
6	1220	99.8	231	5	PCT-US95-03866-6
7	768.5	62.8	235	1	US-08-243-545-6
8	768.5	62.8	235	2	US-08-993-962-6
9	768.5	62.8	235	4	US-09-160-841-6
10	768.5	62.8	235	4	US-09-109-100-1
11	768.5	62.8	235	5	PCT-US94-05365-6
12	724.2	59.2	137	4	US-09-109-100-19
13	692	56.6	212	4	US-09-109-100-10
14	687	56.2	209	4	US-09-109-100-15
15	686	56.1	209	4	US-09-109-100-14
16	685	56.1	209	4	US-09-109-100-18
17	685	56.0	209	4	US-09-109-100-16
18	682	55.8	209	4	US-09-109-100-9
19	682	55.8	209	4	US-09-109-100-12
20	680	55.5	209	4	US-09-109-100-17
21	679	55.5	209	4	US-09-109-100-11
22	679	55.4	209	4	US-09-109-100-13
23	678	55.4	209	4	US-09-109-100-8
24	216	17.7	42	5	PCT-US94-05150-17
25	135	11.0	28	5	PCT-US84-05150-12
26	105	8.6	22	5	PCT-US94-05150-10
27	95.5	7.8	909	2	US-08-310-912A-142

28	95.5	7.8	909	4	US-09-301-085-142	Sequence 142, App
29	95.5	7.8	909	5	PCT-US95-04589-142	Sequence 142, App
30	92	7.5	885	2	US-08-310-912A-2	Sequence 2, Appl1
31	92	7.5	885	3	US-08-841-089-2	Sequence 2, Appl1
32	92	7.5	885	4	US-09-301-085-2	Sequence 2, Appl1
33	92	7.5	885	5	PCT-US95-04570-2	Sequence 2, Appl1
34	92	7.5	885	5	PCT-US95-04589-2	Sequence 2, Appl1
35	83.5	6.8	552	1	US-07-999-280A-22	Sequence 22, Appl1
36	83.5	6.8	552	1	US-07-999-280A-24	Sequence 22, Appl1
37	83.5	6.8	552	1	US-08-426-279-22	Sequence 22, Appl1
38	83.5	6.8	552	1	US-08-426-279-24	Sequence 22, Appl1
39	83.5	6.8	552	1	US-08-401-013-22	Sequence 22, Appl1
40	83.5	6.8	552	1	US-08-401-013-24	Sequence 22, Appl1
41	83.5	6.8	552	3	US-08-426-570-22	Sequence 22, Appl1
42	83.5	6.8	552	3	US-08-426-570-24	Sequence 22, Appl1
43	83.5	6.8	552	3	US-08-426-876-22	Sequence 22, Appl1
44	83.5	6.8	552	3	US-08-426-876-24	Sequence 22, Appl1
45	83.5	6.8	552	4	US-08-426-243-22	Sequence 24, Appl1
46	83.5	6.8	552	4	US-08-426-243-24	Sequence 24, Appl1
47	83.5	6.8	552	4	US-08-401-632-22	Sequence 24, Appl1
48	83.5	6.8	552	4	US-08-401-632-24	Sequence 24, Appl1
49	83.5	6.8	859	3	US-09-183-253-2	Sequence 2, Appl1
50	83.5	6.8	2476	2	US-08-276-967-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-243-545-2
; Sequence 2, Application US/08243545
; Patent No. 5534512
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; TITLE OF INVENTION: Ligands for flk3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-2

Query Match 100.0%; Score 1223; DB 1; Length 231;
Best Local Similarity 100.0%; Pred. No. 6,9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTHLKDYPVT 60
DB 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTHLKDYPVT 60
QY 61 VAVNLODEKCKALMSIFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLODEKCKALMSIFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCPDSTLLPRSPITALEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCPDSTLLPRSPITALEAT 180
QY 181 ELPEPRRQLLLLLLLPLTLVLLAAAGLRWQARRRGELHPGVLPSPHP 231
DB 181 ELPEPRRQLLLLLLLPLTLVLLAAAGLRWQARRRGELHPGVLPSPHP 231

RESULT 2
US-08-993-962-2
Sequence 2, Application US/08993962
Patent No. 5843423
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2613-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-2

Query Match 100.0%; Score 1223; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 6,9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTHLKDYPVT 60
DB 1 MTVLAPAMSPNSLLLLLSPLCLRGTPDCYFSHSPISSNFKVFRRLTHLKDYPVT 60
QY 61 VAVNLODEKCKALMSIFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
DB 61 VAVNLODEKCKALMSIFLAQRWIEOLKTVAGSKMOTLLEDVNTIEHFVTSCTFQPLPEC 120
QY 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCPDSTLLPRSPITALEAT 180
DB 121 LRFVQTNISHLKDTCTQLALKPCIGKACONFSRCLEVOCCPDSTLLPRSPITALEAT 180
QY 181 ELPEPRRQLLLLLLLPLTLVLLAAAGLRWQARRRGELHPGVLPSPHP 231
DB 181 ELPEPRRQLLLLLLLPLTLVLLAAAGLRWQARRRGELHPGVLPSPHP 231

RESULT 3
US-09-160-841-2
Sequence 2, Application US/09160841
Patent No. 6190655
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.

1
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-2

Query Match 100.0%; Score 1223; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLSLILLLSPCLRGTPDCYFHSPISSNFKVFRRLTHLKDYPVT 60
DB 1 MTVALPAMSPNSLSLILLLSPCLRGTPDCYFHSPISSNFKVFRRLTHLKDYPVT 60
QY 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAGSKMOTLLEDVNTFIEHVTSCFQPLPEC 120
DB 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAGSKMOTLLEDVNTFIEHVTSCFQPLPEC 120
QY 121 LRFVQTNISHLKDTQTOLALPKCIGKACQNFSCLEVOQCPDSSITLLPPRSPTALEAT 180
DB 121 LRFVQTNISHLKDTQTOLALPKCIGKACQNFSCLEVOQCPDSSITLLPPRSPTALEAT 180
QY 181 ELPEPRROLILLLPLTVLAAAGLWQARRRGGELHPGVPLPSHP 231
DB 181 ELPEPRROLILLLPLTVLAAAGLWQARRRGGELHPGVPLPSHP 231

RESULT 4
PCT-US94-05365-2
Sequence 2, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05365-2

Query Match 100.0%; Score 1223; DB 5; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.9e-119;
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVALPAMSPNSLSLILLLSPCLRGTPDCYFHSPISSNFKVFRRLTHLKDYPVT 60
DB 1 MTVALPAMSPNSLSLILLLSPCLRGTPDCYFHSPISSNFKVFRRLTHLKDYPVT 60
QY 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAGSKMOTLLEDVNTFIEHVTSCFQPLPEC 120
DB 61 VAVNLODEKHCALWSLFLAQRWIEQLKTVAGSKMOTLLEDVNTFIEHVTSCFQPLPEC 120
QY 121 LRFVQTNISHLKDTQTOLALPKCIGKACQNFSCLEVOQCPDSSITLLPPRSPTALEAT 180
DB 121 LRFVQTNISHLKDTQTOLALPKCIGKACQNFSCLEVOQCPDSSITLLPPRSPTALEAT 180
QY 181 ELPEPRROLILLLPLTVLAAAGLWQARRRGGELHPGVPLPSHP 231
DB 181 ELPEPRROLILLLPLTVLAAAGLWQARRRGGELHPGVPLPSHP 231

RESULT 5
US-08-220-379B-7
Sequence 7, Application US/08220379B
Patent No. 5525708
GENERAL INFORMATION:
APPLICANT: No. 5525708ka, Karl
APPLICANT: Lobell, Robert B
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,379B

FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
PUBLICATION INFORMATION:
AUTHORS: Lyman, et al.
JOURNAL: Cell
PAGES: 1157-1167
DATE: 1993
RELEVANT RESIDUES IN SEQ ID NO: 7: FROM 1 TO 231
US-08-220-379B-7

Query Match 99.8%; Score 1220; DB 1; Length 231;
Best Local Similarity 99.6%; Pred. No. 1,4e-118;
Matches 230; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAPMSNSSLLLLLSPLCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
DB 1 MTVALPAPMSNSSLLLLLSPLCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
QY 61 VAVNLQDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
DB 61 VAVNLQDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
QY 121 LRFQNTISHLKDTCTQLALKPCIGKACQNFSCLEVCQCPDSTLLPRSPALAEAT 180
DB 121 LRFQNTISHLKDTCTQLALKPCIGKACQNFSCLEVCQCPDSTLLPRSPALAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLAAAMGLRWQRRARRGELHPGVLPDPSHP 231
DB 181 ELPEPRRQLLLLLLPLTLVLAAAMGLRWQRRARRGELHPGVLPDPSHP 231

RESULT 6
PCT-US95-03866-6
Sequence 6, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: Cytomed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03866

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220,379
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F.
REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..205
PCT-US95-03866-6

Query Match 99.8%; Score 1220; DB 5; Length 231;
Best Local Similarity 99.6%; Pred. No. 1,4e-118;
Matches 230; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTVALPAPMSNSSLLLLLSPLCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
DB 1 MTVALPAPMSNSSLLLLLSPLCLRGTPDCYFSHSPISSNPKYKFRRLTDHLKDPVPT 60
QY 61 VAVNLQDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
DB 61 VAVNLQDEKHKALMSLFLAQRWIEQDKTVAGSKMOTLLEDVNTIEIHVTSCTFQPLPEC 120
QY 121 LRFQNTISHLKDTCTQLALKPCIGKACQNFSCLEVCQCPDSTLLPRSPALAEAT 180
DB 121 LRFQNTISHLKDTCTQLALKPCIGKACQNFSCLEVCQCPDSTLLPRSPALAEAT 180
QY 181 ELPEPRRQLLLLLLPLTLVLAAAMGLRWQRRARRGELHPGVLPDPSHP 231
DB 181 ELPEPRRQLLLLLLPLTLVLAAAMGLRWQRRARRGELHPGVLPDPSHP 231

RESULT 7
US-08-243-545-6
Sequence 6, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for Flt3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:


```

; APPLICATION NUMBER: US 08/162,407
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: 08/066,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-243-545-6

```

```

Query Match      62.8%; Score 768.5; DB 1; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

```

```

QY 1 MTVLAPAMSPSSLLLLLLLSPLKGTDPDCTFSPHSPISSNFKVFERELTHLKDVPVT 60
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MTVLAPAMSP--TTVL|LL|LL|LL|SSGLSGTDCSPHSPISSDPAVKIRLSPLYLQDVPVT 59

QY 61 VAVN|ODEKHCKALMS|FLAQRWIEQLKTIVAGSKMOTLLEDVNTIEHVTSCFQPLPEC 120
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 60 VASN|ODELGGIMRLV|LAQRWMERLKTIVAGSKMGLLERVNTEHVTFCARQPPESC 119

QY 121 LRFVQTNISHLKDTCTQLLAKPCIGKACONFSRCLEVCOPDSSSTLLPRSPRLAEAT 180
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 120 LRFVQTNISRLQETSQ|VALKFWITR--QNF|SRCL|EQCPDSSSTLLPPWSPRL|EAT 177

QY 181 ELPEPRRQ|LL|LL|LL|PLTVLLAAMGLRMQARRR---GELHPGVLP 228
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 178 APTAQP--L|LL|LL|PVGLLL|LAAMCLHMQRTRRTPRGEGVPPVPS 227

```

```

RESULT 8
US-08-993-962-6
; Sequence 6, Application US/08993962
; Patent No. 5843423
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word, Version #5.1
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/993,962
; FILING DATE: December 18, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,407
; FILING DATE: December 3, 1993
; APPLICATION NUMBER: 08/111,758
; FILING DATE: August 25, 1993
; CLASSIFICATION: 424
; APPLICATION NUMBER: 08/106,463
; FILING DATE: August 12, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/068,394
; FILING DATE: May 24, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2813-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-993-962-6

```

```

Query Match      62.8%; Score 768.5; DB 2; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

```

```

QY 1 MTVLAPAMSPSSLLLLLLLSPLKGTDPDCTFSPHSPISSNFKVFERELTHLKDVPVT 60
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MTVLAPAMSP--TTVL|LL|LL|LL|SSGLSGTDCSPHSPISSDPAVKIRLSPLYLQDVPVT 59

QY 61 VAVN|ODEKHCKALMS|FLAQRWIEQLKTIVAGSKMOTLLEDVNTIEHVTSCFQPLPEC 120
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 60 VASN|ODELGGIMRLV|LAQRWMERLKTIVAGSKMGLLERVNTEHVTFCARQPPESC 119

QY 121 LRFVQTNISHLKDTCTQLLAKPCIGKACONFSRCLEVCOPDSSSTLLPRSPRLAEAT 180
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 120 LRFVQTNISRLQETSQ|VALKFWITR--QNF|SRCL|EQCPDSSSTLLPPWSPRL|EAT 177

QY 181 ELPEPRRQ|LL|LL|LL|PLTVLLAAMGLRMQARRR---GELHPGVLP 228
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 178 APTAQP--L|LL|LL|PVGLLL|LAAMCLHMQRTRRTPRGEGVPPVPS 227

```

```

RESULT 9
US-09-160-841-6
; Sequence 6, Application US/09160841
; Patent No. 6190655
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephen L. Malaska, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO.: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-6

Query Match 62.8%; Score 768.5; DB 4; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72; Mismatches 43; Indels 9; Gaps 4;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MVLAPAWSPNSLLILLSPCLRGTPDCYFHSPISSNFYKFKRELTDHLKDYPT 60
1 MVLAPAWSP-TTYLLILLSSGLSGFQDCSPFHSPISSDFAVKIRELSDYLLQDYPVT 59
DB 61 VAVNLDEKHCRAWSEFLAQRWTEOLTVAGSKMOTLEEVNTEHFVTKCAFQPPPC 120
60 VASNLDEELCGGLWRLVLAQRWTEOLTVAGSKMOTLEEVNTEHFVTKCAFQPPPC 119
QY 121 LRFVQTNISHLKDTCTQLALPCIGRACONFSKCLEVOCOPDSSLPPRSPALEAT 180
120 LRFVQTNISHLKDTCTQLALPCIGRACONFSKCLEVOCOPDSSLPPRSPALEAT 177
DB 181 ELPEPPRROLILLPLTIVLLAAAGLRRORARR---GELHGVPLP 228
178 APTAPQPP-LTLLLLPVGLILLAAWCLHWQRTKRTTPRGQVPPVSP 227

RESULT 10
US-09-109-100-1
Sequence 1, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260, 0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ. ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ. ID NO. 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens

US-09-109-100-1

Query Match 62.8%; Score 768.5; DB 4; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72; Mismatches 43; Indels 9; Gaps 4;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MVLAPAWSPNSLLILLSPCLRGTPDCYFHSPISSNFYKFKRELTDHLKDYPT 60
1 MVLAPAWSP-TTYLLILLSSGLSGFQDCSPFHSPISSDFAVKIRELSDYLLQDYPVT 59
DB 61 VAVNLDEKHCRAWSEFLAQRWTEOLTVAGSKMOTLEEVNTEHFVTKCAFQPPPC 120
60 VASNLDEELCGGLWRLVLAQRWTEOLTVAGSKMOTLEEVNTEHFVTKCAFQPPPC 119
QY 121 LRFVQTNISHLKDTCTQLALPCIGRACONFSKCLEVOCOPDSSLPPRSPALEAT 180
120 LRFVQTNISHLKDTCTQLALPCIGRACONFSKCLEVOCOPDSSLPPRSPALEAT 177
DB 181 ELPEPPRROLILLPLTIVLLAAAGLRRORARR---GELHGVPLP 228
178 APTAPQPP-LTLLLLPVGLILLAAWCLHWQRTKRTTPRGQVPPVSP 227

RESULT 11
PCT-US94-05365-6
Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for FLT3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: -to be assigned-
FILING DATE: May 11, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,502
FILING DATE: March 7, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,407
FILING DATE: December 3, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05365-6

Query Match 62.8%; Score 768.5; DB 5; Length 235;
Best Local Similarity 70.3%; Pred. No. 8e-72;
Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MTVALPAMSPSSLLILLSPCLRTGTPCYFSHPISNFKYKRELTDHLKDYPT 60
D 1 MTVALPAMSP TTYLLLLLLSSGLSTODCSFQHSPISSDFAVKIRELSDYLLQDYPY 59
QY 61 VAVNLQDEKCKALMSLFLAQRMEQLKTVAGSKMOTLEDVNTIEHFVTSCTFQPLPFC 120
D 60 VASNLQDEELGGIMRLVLAQRMMERLKTVAAGSKMOTLEDVNTIEHFVTSCTFQPLPFC 119
QY 121 LRFVOTNISHLKDTCTQLALPKPCIGAKONFSRCLEVOCCOPDSTLLPPSPALFAT 180
D 120 LRFVOTNISHLKDTCTQLALPKPCIGAKONFSRCLEVOCCOPDSTLLPPSPALFAT 177
QY 181 ELPPRRQLLLLLPLTVLLAAMGLRMQRRRR---GELHPGVPLP 228
D 178 APTAPQP-LLLLLLPVGLLLAAMGLRMQRRRRRRRPPRGEQVPVPSP 227

RESULT 12
US-09-109-100-19
Sequence 19, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 19
LENGTH: 137
TYPE: PRT
ORGANISM: Murine
US-09-109-100-19

Query Match 59.2%; Score 724.5; DB 4; Length 137;
Best Local Similarity 99.3%; Pred. No. 1.4e-67;
Matches 136; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 28 TPDCYFSHPISNFKYKRELTDHLKDYPTVAVNLOD-EKHKCALMSFLAQRWIEO 86
D 1 TPDCYFSHPISNFKYKRELTDHLKDYPTVAVNLOD-EKHKCALMSFLAQRWIEO 60
QY 87 LKTVAGSKMOTLEDVNTIEHFVTSCTFQPLPFCRLRFVOTNISHLKDTCTQLALPKCI 146
D 61 LKTVAGSKMOTLEDVNTIEHFVTSCTFQPLPFCRLRFVOTNISHLKDTCTQLALPKCI 120
QY 147 GKACONFSRCLEVOCCOP 163
D 121 GKACONFSRCLEVOCCOP 137

RESULT 13
US-09-109-100-10
Sequence 10, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 10
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-10

Query Match 56.6%; Score 692; DB 4; Length 212;
Best Local Similarity 69.9%; Pred. No. 5.7e-64;
Matches 144; Conservative 15; Mismatches 39; Indels 8; Gaps 3;

QY 27 GTPCYFSHPISNFKYKRELTDHLKDYPTVAVNLODEKCKALMSFLAQRWIEO 86
D 3 GTPDCSFQHSPISSDFAVKIRELSDYLLQDYPYVASNLODEELGGIMRLVLAQRMMER 62
QY 87 LKTVAGSKMOTLEDVNTIEHFVTSCTFQPLPFCRLRFVOTNISHLKDTCTQLALPKCI 146
D 63 LKTVAGSKMOTLEDVNTIEHFVTSCTFQPLPFCRLRFVOTNISHLKDTCTQLALPKCI 122
QY 147 GKACONFSRCLEVOCCOPDSTLLPPSPALFATLPEPRRQLLLLLPLTVLLAA 206
D 123 TR-QNFSRCLEVOCCOPDSTLLPPSPALFATLPEPRRQLLLLLPLTVLLAA 178
QY 207 AWGLRMQRRRR---GELHPGVPLP 228
D 179 AWGLRMQRRRRRRRPPRGEQVPVPSP 204

RESULT 14
US-09-109-100-15
Sequence 15, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 56.2%; Score 687; DB 4; Length 209;
Best Local Similarity 69.8%; Pred. No. 1.9e-63;
Matches 143; Conservative 16; Mismatches 38; Indels 8; Gaps 3;

QY 28 TPDCYFSHPISNFKYKRELTDHLKDYPTVAVNLODEKCKALMSFLAQRWIEO 87
D 1 TPDCSFQHSPISSDFAVKIRELSDYLLQDYPYVASNLODEELGGIMRLVLAQRMMERL 60
QY 88 KTVAGSKMOTLEDVNTIEHFVTSCTFQPLPFCRLRFVOTNISHLKDTCTQLALPKCI 147
D 61 KTVAGSKMOTLEDVNTIEHFVTSCTFQPLPFCRLRFVOTNISHLKDTCTQLALPKCI 120

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7  NUMBER OF LOGS IS 20
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 9
; LENGTH: 209
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-109-100-9

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Query Match	55.8%;	Score 682;	DB 4;	Length 209;
Best Local Similarity	69.38;	Pred. No. 6.1e-63;		
Matches 142;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3;

Qy	28	TPQCVSHSPISNKNFYFRELTHLTKDYPVYAVNLQDEHKCALMSLELAQRNIEOL	87
Db	1	TQDCSHSPISPDPAVYIRELSDYLLQDPYVYASNLQDEELCGMLRYVLAQNNMERL	60
Qy	88	KTVAGSKMOTLLEDVNETIHHVTSCTFROPYDECLRFVQVNIISHLKDPCTOGLAKPCIG	147
Db	61	KVYTSKMGGLLENRTNETHVTKCAQPPSCLRRVQVNIISRLQETSBDYALKRPIT	120
Qy	148	KACQANSRLCEVQCPQDSSTLLPRSPRLATEELDEPPRRQULLLLLPVLVLAAA	207
Db	121	R--QNSRLCEVQCPQDSSTLLPRWSPRLPEATATPAAP--LTLTLPLVGLLLAAA	176
Qy	208	WGLRMQRRARR---GELHPGVPLP	228
Db	177	WCLHMQRRTRRRTPRGEEVPPVPS	201

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RESULT 19
US-09-109-100-12
Sequence 12, Application US/09109100C
Patent No. 629161
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGraw, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03360.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-12

```

Query Match	55.8%;	Score 682;	DB 4;	Length 209;
Best Local Similarity	69.3%;	Pred. No. 6.1e-63;		
Matches 142;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3;

QY	28	TTPCYFSSHPSSNNKVFRELTHLTKRDVPYVAVNADERRKALMSLPAQWIEOL	87
Db	1	TQCSQHSHPSSIDPAAVYIRLSDYFPQDYPAVYASNLQDEELCGGLRWLYLAQRMRRL	60
QY	88	KTVAGSKMOTLLEDVNETIEHFVTCFQPLPECLRLVQVNIISHLKDPCTOYLAKRCIG	147
Db	61	KTVAGSKMGGLLERNETIEIHVTWKCAQPPSCLRRVQVNIISRLQGRISQDVALKRWIT	120
QY	148	KACQANSRLCEVQCPDSSSTLLPRSTLATEATLPEPPRRQULLLLLLLPLTVLLAA	207
Db	121	R-QNSRSLCEIQCPDSSSTLLPRWSSRLPEATAPAPQ--LTLILLPLVGLLLAA	176
QY	208	WGLRWQRAARR---GELHPVPLP	228
Db	177	WCLHMQRTRRRTPRGEQVPPVPS	201

RESULT 20
US-09-109-100-17
; Sequence 17, Application US/09109100C
; Patent No. 6291661

```

: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGraw, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03660.0028
: CURRENT APPLICATION NUMBER: US/09/109,100C
: CURRENT FILING DATE: 1998-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 17
: LENGTH: 209
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-109-100-17

```

Query Match	55.8%;	Score 682;	DB 4;	Length 209;
Best Local Similarity	69.3%;	Pred. No. 6.1e-63;		
Matches 142;	Conservative 16;	Mismatches 39;	Indels 8;	Gaps 3;

QY	28	TPLCQYSHSP	ISSNNKRVFR	RETELTHLTKD	PVYVAVN	MLDDEKHCALMS	SLFLAQRMLEOL	8	
Db	1	TODCSQHSPISSD	PAVNI	RELSDYLLLOD	PVYVAVN	MLDDEELCGGLWR	LYLAORWMBRL	60	
QY	88	KTYAGSMOTL	LEDYNTL	HEHFTSC	FOPLRE	CFRQVNI	SHLTKDTCYOLALKC	147	
Db	61	KTYAGSMQGL	BERVNTL	HEHFTKCAR	QPPSC	FRFQVNI	SHLTKDTS	SEQVYALMKPIT	120
QY	148	KAQONSRL	LEVQCQ	PDSSTLL	PRSPAL	EAELRE	PPRRLOL	LLLLLLPLTYL	207
Db	121	R--RNSRCL	ELQOCQ	DSSTLL	PPRSPAL	EAELRE	PPRRLOL	AAAA	176
QY	208	WGLRWQ	PARRR--	GELH	PGVPLP				
Db	177	WCLHMQR	TRRRRT	PRQEGV	PPVPSP				

```

RESULT 21
US-09-109-100-11
Sequence 11, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ. ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-11

```

Query Match	55.68;	Score 680;	DB 4;	Length 209;
Best Local Similarity	69.38;	Pred. No. 9.8e-63;		
Matches 147;	Conservative 16;	Mismatches 39;	Indels 8;	Gaps 3;

[illegible]

```

QY      208 WGLRWQRARR---GELHPGVPLP 228
          | | | | | | | | | |
Db      177 WCLHWQTRRRTPRPGEQVPVPSP 201

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1 RESULT 22
2 US-09-109-100-13
3 : Sequence 13, Application US/09109100C
4 : Patient No. 6291661
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Graddis, Thomas J.
9 : APPLICANT: McGraw, Jeffrey T.
10 : TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
11 : FILE REFERENCE: 03360, 0028
12 : CURRENT APPLICATION NUMBER: US/09/109,100C
13 : CURRENT FILING DATE: 1998-07-02
14 : NUMBER OF SEQ ID NOS: 20
15 : SOFTWARE: PatentIn Ver. 2.1
16 : SEQ ID NO 13
17 :
18 : LENGTH: 209
19 :
20 : TYPE: PRT
21 :
22 : ORGANISM: Homo sapiens
23 :
24 : US-09-109-100-13

```

Query Match	55.58;	Score 679;	DB 4;	Length 209;
Best Local Similarity	69.38;	Pred. No. 1.2e-62;		
Matches 14;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3

QY	28	TTCGYSHPISNFKVFEETLTHLKDDPVVAVALDECKKMLMSFLAOWMIOL	87
Db	1	TQCCSQHPISSDPAVKIKRELSDTLRODIPVYVASTLQDEELCGELMRVLVLAQRMHERL	60
QY	88	KTVAGSKMOTLEDVNTLEIHFVTSCTOPRPECIRFVQVNISSHLDKTCYOLALPKCIG	147
Db	61	KTVAGSKMGGLLEARNTEIHFVTKCAQORPPSCIRFQVNISSHLQENSEGVALKAPIT	120
QY	148	KACQNSKCLEVFQCPDSDSTLLPPRSPLAEALDELPERRPROLLMLPLTVLAAA	207
Db	121	R-QNSKCLEIQCOPDSDSTLLPPMSPPRPLEATAFAPQPR-LTLLILLPLVGLILLAAA	176
QY	208	NGLRMQRRRR-----GELHPGVRPLP	228
Db	177	WCLHMQRTRRRKTPRPEGVOVPPVPS	201

```

1  RESULT 23
2  US-09-109-100-8
3  : Sequence 8, Application US/09109100C
4  : Patient No. 6291661
5  :
6  : GENERAL INFORMATION:
7  : APPLICANT: GRADDIS, Thomas J.
8  : APPLICANT: McGREW, Jeffrey T.
9  : TITLE OF INVENTION: FL73-L MUTANTS AND METHODS OF USE
10 : FILE REFERENCE: 03260, 0028
11 : CURRENT APPLICATION NUMBER: US/09/109,100C
12 : CURRENT FILING DATE: 1998-07-02
13 : NUMBER OF SEQ ID NOS: 20
14 : SOFTWARE: PatentIn Ver. 2.1
15 : SEQ ID NO 8
16 :
17 : LENGTH: 209
18 :
19 : TYPE: PRT
20 :
21 : ORGANISM: Homo sapiens
22 :
23 : US-09-109-100-8

```

Query Match	55.4%;	Score 678;	DB 4;	length 209;
Best Local Similarity	69.3%;	Pred. No. 1.6e-62;		
Matches 142;	Conservative 15;	Mismatches 40;	Indels 8;	Gaps 3

[illegible]

Oy	88	KTVAGSMOILEDVNTETHEFTSTCPDLEPCRCFQVTNSHLKTCOLATLAPCIG	147
Dz	61	KTVAGSMGOLLERVNTETHEFTVKCAFQPPSCSRFQVTNIRLOQTSPQIALKPWIT	120
Oy	148	KACONSRCICEVOCCDSSTLLPRSPALANTELPEPRPQULIIILLLLPLVLVLAHA	207
Dz	121	R-QNRSRCLIEDCOVDSDSTLLPPMSPRLINRTAPTARPP--TLILLLLPVGLLLLLAAH	176
Oy	208	WGLRWDQARRR---GELHPGVLP	228
Dz	177	WCLHMQRTRRRRPREGVOYEVFPSP	201

```

: RESULT 24
: PCT-US94-05150-17
: Sequence 17, Application PC/TUS9405150
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Purified Mammalian Flt3 Ligands and Agonists and Antagonists
: NUMBER OF SEQUENCES: 37
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: Macintosh 6.0.5
: SOFTWARE: Microsoft Word 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/05150
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/162,413
: FILING DATE: 03-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/155,111
: FILING DATE: 19-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/112,391
: FILING DATE: 24-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/106,340
: FILING DATE: 13-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/092,549
: FILING DATE: 16-JUL-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/089,263
: FILING DATE: 07-JUL-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/065,231
: FILING DATE: 19-MAY-1993
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: PCT-US94-05150-17

```

Query Match	17.78;	Score 216;	DB 5;	Length 42;
Best Local Similarity	97.68;	Pred. No. 1.2e-15;		
Matches 4;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

```

RESULT 25
PCT-US94-03150-12
; Sequence 12, Application PC/TUS9405150
; GENERAL INFORMATION:
QY      28 TDDCYFHSNPISNNFVKRELTLLKDDPVYVAVNLODER 6
Db      1 TDDCYFHSNPISNNFVKRELTLLKDDPVYVAVNLODER 4

```

APPLICANT:
APPLICANT:
TITLE OF INVENTION: Purified Mammalian Flt3 Ligands and Agonists and Antagonists
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05150
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/092,549
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-05150-12

Query Match 11.0%; Score 135; DB 5; Length 28;
Best Local Similarity 92.9%; Pred. No. 1.6e-07;
Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 28 TPDCYFSHSPISSNFKYKFRRLDHLK 55
DB 1 TPDAFSSHPISSNFKYKFRRLDHLK 28

Search completed: August 6, 2002, 09:39:38
Job time: 269 sec

